

GenCore version 5.1.3
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in - protein search, using sw model

November 25, 2002, 09:59:40 ; Search time 36 seconds
(without alignments)
736.580 Million cell updates/sec

US-09-785-738A-2

score:

1097
a: 1 MENEFDGKTEVLEAWYDD.....KEFLAKLLKSGENQAVEGF 199

table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

d: 908470 seqs, 133250620 residues

number of hits satisfying chosen parameters: 908470

n DB seq length: 0

n DB seq length: 2000000000

rocessing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Alt to.	Score	Query Match	Length	ID	Description
1	1097	100.0	199	AAE08929	Rice submergence-i
2	955.5	87.1	198	AAE08930	Rice submergence-i
3	862	78.6	200	AAE08934	Cotton submergence
4	833.5	76.0	199	AAE08935	Arabidopsis thalia
5	833.5	76.0	199	AAE08935	Arabidopsis thalia
6	833.5	76.0	438	AAE08935	Arabidopsis thalia
7	833.5	76.0	495	AAE08935	Arabidopsis thalia
8	833.5	76.0	512	AAE08935	Arabidopsis thalia
9	838	75.5	192	AAE08935	Arabidopsis thalia
10	814	74.2	559	AAU72532	Arabidopsis cell c

11	812	74.0	196	AAE08931	Tomato submergence
12	800	72.9	198	AAE08931	Arabidopsis thalia
13	789.5	72.0	940	AAE08931	Arabidopsis thalia
14	782.5	71.3	182	AAE08931	Arabidopsis thalia
15	782.5	71.3	182	AAE08931	Arabidopsis thalia
16	781	71.2	199	AAE08931	Arabidopsis thalia
17	779	71.0	210	AAE08933	Soybean submergence
18	776	70.7	175	AAE08933	Arabidopsis thalia
19	776	70.7	175	AAE08933	Arabidopsis thalia
20	751	68.5	181	AAE08933	Arabidopsis thalia
21	737.5	67.2	923	AAE08933	Tomato submergence
22	691	63.0	189	AAE08932	Arabidopsis thalia
23	690	62.9	187	AAE08932	Arabidopsis thalia
24	690	62.9	199	AAE08932	Arabidopsis thalia
25	684	62.4	187	AAE08932	Arabidopsis thalia
26	684	62.4	198	AAE08932	Arabidopsis thalia
27	665	60.6	180	AAE08932	Arabidopsis thalia
28	659	60.1	180	AAE08932	Arabidopsis thalia
29	609	55.5	184	AAE08936	Mouse submergence-
30	586	53.4	191	AAE08936	Human protein seq
31	586	53.4	206	AAE08936	Human cancer assoc
32	586	53.4	206	AAE08936	Human ovarian anti
33	586	53.4	209	AAE08936	Human protein seq
34	581.5	53.0	181	AAE08937	zebrafish submerge
35	581	53.0	179	AAE08937	Human protein sequ
36	568	51.8	149	AAE08937	Arabidopsis thalia
37	568	51.8	866	AAE08937	Arabidopsis thalia
38	558	50.9	173	AAE08937	Human shear stress
39	542.5	49.5	125	AAE08937	Arabidopsis thalia
40	542.5	49.5	125	AAE08937	Arabidopsis thalia
41	542.5	49.5	125	AAE08937	Arabidopsis thalia
42	539.5	49.2	187	AAE08935	Human submergence-
43	535	48.8	118	AAE08935	Arabidopsis thalia
44	534.5	48.7	125	AAE08935	Arabidopsis thalia
45	529	48.2	124	AAE08935	Arabidopsis thalia

ALIGNMENTS

RESULT 1

AAE08929
ID AAE08929 standard; Protein; 199 AA.

XX AAE08929;

XX AC

XX 15-NOV-2001 (first entry)

DE Rice submergence-induced early response protein SH2A.
XX Rice; SH2A; submergence induced early response gene; anaerobic response;
KW water logging tolerance; hypoxic environment; horticultural;
KW agricultural; medical; fermentation; cell culture industry;
KW genetic construct; transgenic plant.

OS Oryza sativa.

XX Key

FT Modified-site 21..24 Location/Qualifiers

FT /label= CK2 /note= "Casein kinase II phosphorylation site"

FT Modified-site 49..51 /label= PKC

FT /note= "Protein kinase C phosphorylation site"

FT Region 64..67 /note= "Nuclear localisation signal"

FT Modified-site 64..72 /label= TYR

FT /note= "Tyrosine kinase phosphorylation site"

FT Modified-site 73..76 /label= CK2

FT /note= "Casein kinase II phosphorylation site"

FT Modified-site 94..97

/label= CK2
/note= "Casein kinase II phosphorylation site"
102..105
Modified-site
/label= CK2
/note= "Casein kinase II phosphorylation site"
107..115
Modified-site
/label= TYR
/note= "Tyrosine kinase phosphorylation site"
145..152
Region
/label= Destruction_box
/note= "The presence of a destruction box motif
indicates that the protein undergoes rapid
turnover, which is a means of regulating its
activity"
145..153
Modified-site
/label= TYR
/note= "Tyrosine kinase phosphorylation site"
189..192
Modified-site
/label= CK2
/note= "Casein kinase II phosphorylation site"

WO200161020-A2.

23-AUG-2001.

16-FEB-2001; 2001WO-1B00745.

18-FEB-2000; 2000US-0183572.

(CROP-) CROPDESIGN NV.

Sauter MM, Lorbiecke R;

WPI; 2001-529915/58.

N-PSDB; AAD15647.

New genetic constructs, comprising the SH2A or SH2A-like genes, useful
for altering the growth and adaptation of plants under hypoxic
conditions, e.g. improving water logging tolerance or regulating
anaerobic response in plants -

Example 2; Page 91-92; 107pp; English.

The present invention relates to genetic constructs, which comprise a
nucleotide sequence for an SH2A or SH2A-like gene, or an SH2A or SH2A-
like protein gene promoter, where the SH2A or SH2A-like gene is operably
linked to a promoter sequence that directs expression of the nucleotide
sequence and the SH2A or SH2A-like protein gene promoter is operably
linked to a heterologous coding sequence. The SH2A gene, initially
identified in rice plants, is a submergence-induced early response gene
which is involved in the adaptation of plants to hypoxic conditions
(such as those encountered during submersion). In addition, the SH2A gene
product has also been found to belong to a family of highly conserved
proteins which occur ubiquitously in eukaryotes. The genetic constructs
and methods are useful for altering the growth and adaptation of plants
under hypoxic conditions. In particular, these are useful for improving
water logging tolerance and regulating anaerobic response in plants.
These are particularly useful in horticultural, agricultural, medical,
fermentation and cell culture industries. The present sequence is rice
SH2A protein.

sequence 199 AA;

Y Match 100.0%; Score 1097; DB 22; Length 199;
Local Similarity 100.0%; Pred. No. 5.1e-112;
hes 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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1 MENEFOGKTEVTEAWYMDSEDDQRLPHHREPKFIPVDKLTGLGVSRLNPDNWNVC 60

61 ENLKRIEARGYSVDICDVCPEKLPNYETKIKSFEEHLHTEDEIRYCLGSGYFDVRD 120
|||||

Db 61 ENLKRIEARGYSVDICDVCPEKLPNYETKIKSFEEHLHTEDEIRYCLGSGYFDVRD 120
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Db 121 ONDOWIRIALKKGMIVLPGMYHRTLTDTNVIKAMRLFVGDPVWTPYINRPHDLPARK 180
QY 181 EFLAKLLKSEGENQAVEGF 199
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Db 181 EFLAKLLKSEGENQAVEGF 199
RESULT 2
AAE08930
ID AAE08930 standard; Protein; 198 AA.
XX
AC AAE08930;
XX
DT 15-NOV-2001 (first entry)
XX
DE Rice submergence-induced early response protein SH2B.
XX
KW Rice; SH2A; submergence induced early response gene; anaerobic response;
water logging tolerance; hypoxic environment; horticultural;
agricultural; medical; fermentation; cell culture industry;
genetic construct; transgenic plant; EST S2993; expressed sequence tag.
XX
OS Oryza sativa.
XX
PW WO200161020-A2.
XX
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-1B00745.
XX
PR 18-FEB-2000; 2000US-0183572.
XX
PA (CROP-) CROPDESIGN NV.
XX
PI Sauter MM, Lorbiecke R;
XX
DR WPI; 2001-529915/58.
XX
N-PSDB; AAD15647.
XX
PT New genetic constructs, comprising the SH2A or SH2A-like genes, useful
for altering the growth and adaptation of plants under hypoxic
conditions, e.g. improving water logging tolerance or regulating
anaerobic response in plants -
XX
PS Example 3; Page 93-94; 107pp; English.
XX
CC The present invention relates to genetic constructs, which comprise a
nucleotide sequence for an SH2A or SH2A-like gene, or an SH2A or SH2A-
like protein gene promoter, where the SH2A or SH2A-like gene is operably
linked to a promoter sequence that directs expression of the nucleotide
sequence and the SH2A or SH2A-like protein gene promoter is operably
linked to a heterologous coding sequence. The SH2A gene, initially
identified in rice plants, is a submergence-induced early response gene
which is involved in the adaptation of plants to hypoxic conditions
(such as those encountered during submersion). In addition, the SH2A gene
product has also been found to belong to a family of highly conserved
proteins which occur ubiquitously in eukaryotes. The genetic constructs
and methods are useful for altering the growth and adaptation of plants
under hypoxic conditions. In particular, these are useful for improving
water logging tolerance and regulating anaerobic response in plants.
These are particularly useful in horticultural, agricultural, medical,
fermentation and cell culture industries. The present sequence is a rice
SH2A-like protein, SH2B, encoded by EST (expressed sequence tag) S2993.
XX
SQ Sequence 198 AA;
Query Match 87.1%; Score 955.5; DB 22; Length 198;
Best Local Similarity 85.3%; Pred. No. 1.7e-96;
Matches 168; Conservative 19. Mismatches 1

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21-MAY-1999; 99US-0135353.
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PR 29-OCT-1999; 99US-0162142.

Query Match 76.0%; Score 833.5; DB 21; Length 199;
Best Local Similarity 76.5%; Pred. No. 4.3e-83;
Matches 143; Conservative 29; Mismatches 14; Indels 1; Gaps 1;

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Db 6 KDGREEVIAWYMDSEEDORLPHHDPKEFLSLDKLAELGVLSWRLDADNYETDEDLKK 65
QY 66 IREARGSYVDICDVCPEKLPNYETKIKSFEEHLHTDEIRYCLEGSGYFVDRDNDOW 125
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Db 186 FVKVNEG 192

RESULT 6
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XX
AC AAG45259;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 56796.
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
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XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
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PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
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AAG45299;				
18-OCT-2000 (first entry)				
Arabidopsis thaliana protein fragment SEQ ID NO: 56853.				
Protein identification; signal transduction pathway; metabolic pathway;				
hybridisation assay; genetic mapping; gene expression control; promoter;				
termination sequence.				
Arabidopsis thaliana.				
EP1033405-A2.				
06-SEP-2000.				
25-FEB-2000; 2000EP-0301439.				
25-FEB-1999; 99US-0121825.				

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PR 01-NOV-1999; 99US-0161360.
PR 02-NOV-1999; 99US-0161361.
PR 03-NOV-1999; 99US-0161920.
PR 04-NOV-1999; 99US-0161921.
PR 05-NOV-1999; 99US-0161993.
PR 06-NOV-1999; 99US-0162142.

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Best Local Similarity 76.5%; Pred. No. 1.6e-82;
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QY 61 ENLKRIEARGSYVDICDVCPEKLPNETKIKSFEEHLHTDEEIRYCLEGGYFDVRD 120
DB 61 EDLKKIRRESRGYSYMDFCVCEPKLPNEYKVKSFEEHLHTDEEIRYCVAGTYFDVRD 120
QY 121 QNDQWIRIALKKGGMIVLPAGMYHRTLTQDNVYKAMRLFVGDVPWTPYNNRPHDLPAK 180
DB 121 RNEAWIRVLVKGGMIVLPAGMYHRTLTQDNVYKAMRLFVGDVPWTPYNNRPHDLPAK 180
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DB 181 EYV 183

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AC AAU72532;
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DT 26-FEB-2002 (first entry)
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KW Cell cycle protein; CCP; cell cycle regulation; herbicide;
KW plant growth regulator; plant development; abiotic stress; biotic stress;
KW nutrient deprivation; pathogen attack; crop yield; immunogen.
XX
OS Arabidopsis thaliana.
XX
PN W0200185946-A2.
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Y 187 LKSEGENQAV 196
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b 183 VNADGAGRAV 192

3SULT 12
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17-OCT-2000 (first entry)

Arabidopsis thaliana protein fragment SEQ ID NO: 32943.

Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
termination sequence.

Arabidopsis thaliana.

EP1033405-A2.

06-SEP-2000.

25-FEB-2000; 2000EP-0301439.

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1	MGEAVKDGXEEVIAWYMDSEEDQRLPHIREKEFTIPVDKLTGELGVISRLNPDWENC	60			
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61 ENLAKIRREARCSYV-----DICDVCPEKLPNYETKIKSFFEEHLHTDEIRYCVAGSG 114


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92  IKSFEELHHTDEIRYCLSGSYEDVRDQNDQWIRALKKGMIVLPAGMYHRTFLDLD 151
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      hybridisation assay; genetic mapping; gene expression control; promoter;
      termination sequence.
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      25-FEB-2000; 2000EP-0301439.
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Query Match 71.3%; Score 782.5; DB 21; Length 182;
Best Local Similarity 77.1%; Pred. No. 1.5e-77;
Matches 135; Conservative 26; Mismatches 13; Indels 1; Gaps 1;

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RESULT 15
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DT 18-OCT-2000 (first entry)
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Query Match      71.3%; Score 782.5; DB 21; Length 182;
Best Local Similarity 77.1%; Pred. No. 1.5e-77;
Matches 135; Conservative 26; Mismatches 13; Indels 1; Gaps 1;

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GenCore version 5.1.3
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SUMMARIES

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2	586	53.4	179	4	US-09-234-613-28			Sequence 28, Appl
3	439.5	40.1	163	4	US-09-348-265-2			Sequence 2, Appl
4	94.5	8.6	749	4	US-09-562-737-96			Sequence 96, Appl
5	84	7.7	323	4	US-09-237-543-6			Sequence 6, Appl
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21	77	7.0	313	4	US-09-644-450-7			Sequence 7, Appl
22	77	7.0	318	4	US-09-134-001C-3603			Sequence 3603, Ap
23	76	6.9	571	1	US-07-955-305A-25			Sequence 25, Appl
24	75.5	6.9	749	4	US-09-562-737-99			Sequence 99, Appl
25	75.5	6.9	1138	4	US-09-580-101A-8			Sequence 8, Appl
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35	71	6.5	348	4	US-09-671-950-10			Sequence 10, Appl
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ALIGNMENTS

RESULT 1
US-08-933-750C-28
; Sequence 28, Application US/08933750C
; Patent No. 5932442
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LNOBNOT03

CLONE: 1577239
US-08-933-750C-28

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RESULT 2
US-09-234-613-28
Sequence 28, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Young, Janice
APPLICANT: Yue, Henry
APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:

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TOPOLOGY: linear
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RESULT 3
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Sequence 2, Application US/09348265
Patent No. 6444800
GENERAL INFORMATION:
APPLICANT: KIKUCHI, Kokichi
APPLICANT: SATO, No. 6444800iyuki
APPLICANT: TORIGOE, Toshihiko
APPLICANT: SAHARA, Hiroeki
APPLICANT: SUZUKI, Manabu
APPLICANT: HAMURO, Junji
TITLE OF INVENTION: Human Gastric Cancer Antigen Gene and Gastric
FILE REFERENCE: OP871
CURRENT APPLICATION NUMBER: US/09/348,265
EARLIER FILING DATE: 1999-07-07
EARLIER APPLICATION NUMBER: JP 10-197852
EARLIER FILING DATE: 1998-07-13
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
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DB 120 MEKGMVTLPGIYHRTVDENKNTKAMRLVCG 152

RESULT 4
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Sequence 96, Application US/09562737
Patent No. 6428967
GENERAL INFORMATION:
APPLICANT: Herz, Joachim
APPLICANT: Gotthardt, Michael
TITLE OF INVENTION: LDL Receptor Signaling Pathways
FILE REFERENCE: UTSW0708
CURRENT APPLICATION NUMBER: US/09/562,737
CURRENT FILING DATE: 2000-05-01
NUMBER OF SEQ ID NOS: 1

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ER INFORMATION: Description of Artificial Sequence: Synthetic
ER INFORMATION: Sequence
62-737-96

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9 KTEVIEAWYDDSEEDORLPHHREPK---EFIPVDKLTGELGIVSKLNPDNW---ENC 60
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5 KAESVSGMGLDDRRVPGVPVPEHQPESEDEMF--PLGVYPEGELAAALRPESHAPEQEC 63
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61 ENLKRIREARGYSYVDICDVCPEKLPNYETKIKSFEEHLHDFE-----IRYCLEGGSY 115
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64 HNIS-----PDGSSSDKVN--TSEEDLDEGLPEEEEMITYIRYCPNDOSY 110
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116 FDVROQN--DOMIRIALKKGMIVLPGAGMYHRTLDNYIKAMRLFGVDPWTPYRNPHD 174
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :
111 LEGMQNGEYL-----AHSRHPVDIDECQSAVE-----EWTSATPAP 149
||| : : : ||| : : : ||| : : : ||| : : : ||| : : : ||| : : :

175 H 175
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T 5
-237-543-6
-ence 6, Application US/09237543A
ent No. 6143540
ERAL INFORMATION:
'PLICANT: Kapeller, Rosana
ITLE OF INVENTION: NOVEL MOLECULES OF THE HK1D-1-RELATED PROTEIN FAMILY
ILE REFERENCE: 035800/175631
URRENT APPLICATION NUMBER: US/09/237,543A
URRENT FILING DATE: 1999-01-26
UMBER OF SEQ ID NOS: 11
FTWARE: Patentin Ver. 2.0
Q ID NO 6
LENGTH: 323
TYPE: PRT
ORGANISM: Xenopus laevis
J9-237-543-6

Jery Match          7.78;  Score 84;  DB 4;  Length 323;
est Local Similarity 24.28;  Pred. No. 0.24;
atches 37;  Conservative 27;  Mismatches 57;  Indels 32;  Gaps
99

33  KPEIPVDKLTE-----LGVISWRNLNDW-----ENCENLKIREARGYSVVDICVCE 83
88  PLEIVLLKKVPTAFRGVILNDWVERPDALFLVNERPEPVK-----DLDFVITE 136

84  KLPNYETKIKSFEELHTDEIRYCLE- GSGYFDVRDNDQWIRALKKG--GMIVLPA 140
137  KGPLDEDTARGFPRQVL----EAVRHCTYNGCVVHARDIKDEN---LLVDTRNGELKIDFGS 190

141  GMYHREFLDTDINIKAMRLFVGDPVWTPYNRPH 173

191  GALLKDPVYTD--FDGTRVY-SPPEWRYRYH 220

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SULT 6
-09-644-450-6
Sequence 6, Application US/09644450
Patent No. 6383791
GENERAL INFORMATION:
APPLICANT: Kapeller, Rosana
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY

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; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 035600/175631
; CURRENT APPLICATION NUMBER: US/09/644,450
; CURRENT FILING DATE: 2000-08-23
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 323
; TYPE: PRT
; ORGANISM: Xenopus laevis
US--09-644-450-6

Query Match          7.78; Score 84; DB 4; Length 323;
Best Local Similarity 24.28; Pred. NO. 0.24;
Matches 37; Conservative 27; Mismatches 57; Indels 32; Gaps 9;

QY   33 PKFEIPVOKLTE-----LGVISWRLNPDNW----ENCENLKRIREARGYSYVDICDVCE 83
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB   88 PLEIVLLKKVPFAPRGVINLLDWTERPDAELVMRPEPVK-----DLFDYTE 136

QY   84 KLPNYETKIKFFERHLHTDEIIRYCYLE-CGSGFYDVRDNDQOWIRIALKKG--GMIVLPA 140
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB   137 KGPLDEDTRAFGEFRVL---EAVRHCVCGVHHDIKDEN---LYDYTFNGELKLIDFGS 190

QY   141 GMVHRFTLDTONYIKAMRLFVGDPVPTPNRP 173
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB   191 GALLKDTVTD--FDGTRY--SPPEWRYHYRH 220

RESULT 7
US-08-463-081B-26
; Sequence 26, Application US/08463081B
; Patent No. 5871960 5837487
; GENERAL INFORMATION:
; APPLICANT: Smith, Kendall A. & Beadling, Carol
; TITLE OF INVENTION: Nucleic Acids Encoding CR5 Polypeptide,
; VECTOR AND TRANSFORMED CELL THEREOF, AND EXPRESSION THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
; STREET: 444 South Flower St. - Suite 1900
; CITY: Los Angeles
; STATE: California
; COUNTRY: USA
; ZIP: 90071
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0,
; SOFTWARE: Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/463,081B
; FILING DATE: 5-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/104,736
; FILING DATE: 10-AUG-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/796,066
; FILING DATE: 20-NOV-91
; ATTORNEY/AGENT INFORMATION:
; NAME: Viviana Amzel, Ph. D.
; REGISTRATION NUMBER: 30,930
; REFERENCE/DOCKET NUMBER: P66 38150 (DART-060)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (213) 622-7700
; TELEFAX: (213) 489-4210
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 313 amino acids
; TYPE: amino acid
; STRANDEDNESS: n.a.
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[illegible]

3-074B-26
Se 26, Application US/08463074B
NO. 6020155

AL INFORMATION:
LICANT: Smith, Kendall A. & Beadling, Carol
LE OF INVENTION: Nucleic Acids Encoding CRI Fusion Protein, Vector an
BER OF SEQUENCES: 35
'RESPONSE ADDRESS:
ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
ADDRESSER: (B) STREET:
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90071

MUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
SOFTWARE: Version #1.25
JRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,074B
FILING DATE: 5-JUN-1995
RIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/104,736
FILING DATE: 10-AUG-1993
'RIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/796,066
FILING DATE: 20-NOV-91
ATTORNEY/AGENT INFORMATION:
NAME: Viviana Amzel, Ph. D.
REGISTRATION NUMBER: 30,930
REFERENCE/DOCKET NUMBER: P66 38143 (DART-020)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 622-7700
TELEFAX: (213) 489-4210
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 313 amino acids
TYPE: peptide
STRANDEDNESS: n.a.
TOPOLOGY: n.a.
MOLECULE TYPE: peptide
8-463-074B-26

very Match 7.4%; Score 81; DB 3; Length 313;
st Local Similarity 25.2%; Pred. No. 0.5;
atches 39; Conservative 29; Mismatches 55; Indels 32; Gaps 9;

31 REPKEFIIPVDKLT-----LGVLSWRNLNDW---ENCNLSKRIRARGYSYVDICDVC 81
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85 RVPMEVLLKKVSGFSGVRILLDMWERDSEVLILEREPEVO-----DLDFDI 133
| | | | | : | : | : | : | : | : | : |
82 PEKLPNYETTKTSFEHLHTDEIERYCLE-GSGFYDVDDQNDQWIRIALKG--GMIVL 138
| | | | | : | : | : | : | : | : | : |
134 TERGAQLQEASRFQVWL---BAVRHCNCGLVHRDKDEN---ILIDLNRGELKLIDF 187
| | | | | : | : | : | : | : | : | : |
139 PAGMYHRRFTLOTNYIKAMRLFVGDFVWTPTNRP 173
| | | | | : | : | : | : | : | : | : |
188 GSGALLKDVTVD--FDGTRVY-SPPEWIRYHYH 219
| | | | | : | : | : | : | : | : | : |

LT 11
8-465-585C-26
quence 26, Application US/08465585C
tent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadling, C.
TITLE OF INVENTION: Nucleic Acids Encoding CR6 Polypeptide, Vecto
TITLE OF INVENTION: Transformed Cell Thereof, and Expression Thereof

SUPP. 17

COL. 1
-08-465-585C-26
Sequence 26, Application US/08465585C
Patent No. 6027914
GENERAL INFORMATION:
APPLICANT: Smith, K. A., & Beadli
TITLE OF INVENTION: Nucleic Acids
TITLE OF INVENTION: Transformed C

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1  NUMBER OF SEQUENCES: 35
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
4  ADDRESSEE: (B) STREET:
5  CITY: Los Angeles
6  STATE: California
7  COUNTRY: USA
8  ZIP: 900071
9  COMPUTER READABLE FORM:
10 MEDIUM TYPE: Floppy disk
11 COMPUTER: IBM PC compatible
12 OPERATING SYSTEM: PC-DOS/MS-DOS
13 SOFTWARE: PatentIn Release #1.0, Version #1.25
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/08/465,585C
16 FILING DATE: 5-JUNE-1995
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: USSN 08/330,108
19 FILING DATE: 27-OCT-1994
20 APPLICATION NUMBER: USSN 09/104,736
21 FILING DATE: 10-AUG-1993
22 APPLICATION NUMBER: USSN 07/796,066
23 FILING DATE: 20-NOV-1991
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Viviana Amzel, Ph. D.
26 REGISTRATION NUMBER: 30,930
27 REFERENCE/DOCKET NUMBER: P66 38149 (DART-050)
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (213) 622-7700
30 TELEFAX: (213) 4894210
31 INFORMATION FOR SEQ ID NO: 26:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 313 amino acids
34 TYPE: peptide
35 STRANDEDNESS: n.a.
36 TOPOLOGY: n.a.
37 MOLECULE TYPE: peptide
38
39 US-08-465-585C-26
40
41 Query Match 7.4%; Score 81; DB 3; Length 313;
42 Best Local Similarity 25.2%; Pred. N.0.5;
43 Matches 39; Conservative 29; Mismatches 55; Indels 32; Gaps 9;
44
45 QY 31 REPEETPVOKLTE----LGVISRLRPDWM---ENCENLKRIAREARGYSVDICDVC 81
46 DB 85 RYPMVEVLKKKSGSGSVIRLLDWFERDSEVLILRPPVQ-----DLDFDI 133
47 QY 82 PEKLPNVTETIKSFEELHHTDEETIKYCLE--GSGYFDVRDNDOWIRIAKKG--GMIVL 138
48 DB 134 TERGALQELARSFPEQVL---EAVRHCHNCVLHROIKDEN---ILLDLNRGELKLLDF 187
49 QY 139 PAGMYHRTLDITDNYIKAMRLFVGDPVTPYRNP 173
50 DB 188 GSGALLKDTVYTD--PDGTRVY--SPPEWIRYRHYH 219
51
52 RESULT 12
53 US-08-652-446-26
54 ; Sequence 26, Application US/08652446
55 ; Patent No. 6057427
56 ; GENERAL INFORMATION:
57 ; APPLICANT: Smith, Kendall A. & Beadling, Carol
58 ; TITLE OF INVENTION: Nucleic Acids Encoding CR5
59 ; POLYPEPTIDE: Polypeptide, Vector and Transformed Cell Thereof, and
60 ; TITLE OF INVENTION: Expression Thereof
61 ; NUMBER OF SEQUENCES: 38
62 ; CORRESPONDENCE ADDRESS:
63 ; ADDRESSEE: PRETTY, SCHROEDER & POPLAWSKI
64 ; CITY: Los Angeles
65 ; STATE: California
66 ; COUNTRY: USA
67 ; ZIP: 900071
68
69 444 South Flower St. - Suite

```



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No. 6383791
- INFORMATION:
JANT: Kapellier, Rosana
OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY
OF INVENTION: AND USES THEREOF
REFERENCE: 035800/175631
NT APPLICATION NUMBER: US/09/644,450
NT FILING DATE: 2000-08-23
R OF SEQ ID NOS: 11
ARE: Patentin Ver. 2.0
      NO 8
      MH: 313
      PT: PRT
      ANISM: Rattus norvegicus
      14-450-8

Match          7.4%; Score 81; DB 4; Length 313;
Local Similarity 25.2%; Pred. No. 0.5;
es 39; Conservative 29; Mismatches 55; Indels 32; Gaps 9;

31 REPKEFIVDRKLT-----LGVSLRNLPPDNW----ENCENLKRIRREARGSYVDICDVC 81
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85 RVPMEVLLKKVSGSGFVIRLLDNFEPDSFVILLERPEPVQ-----DLDFDI 133
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82 PEKLPNYETKISPFEEHLHTDEETRYCLE--GSGYFVDRDQNDQIRIALKKG--GMIVL 138
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
134 TERGALOELARSEFQVL--EAVRHCHNGCVLHRDKDEN---ILLDLNARGELKLIDF 187
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
139 PAGMWHRFTLTDQNYIKAMRLFVGDVPTPNRPH 173
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
188 GSGALLKDTVYTD--FDGTRVY--SPPEWIRYHRYH 219
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! completed: November 25, 2002, 10:10:42
! time: 17 secs

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GenCore version 5.1.3
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in - protein search, using sw model

November 25, 2002, 10:10:00 : Search time 10 seconds
(without alignments)
311.664 Million cell updates/sec

US-09-785-738A-2

score: 1097
e: 1 MENEFDGKTEVIAWYMD...KEFLAKLLKSEGENOAVEGF 199

table: BL0SUM62
Gapop 10.0 , Gapext 0.5

id: 100480 seqs, 15651496 residues

number of hits satisfying chosen parameters: 100480

m DB seq length: 0

m DB seq length: 2000000000

processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

18a: Published Applications, AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US05_NEW_PUB pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1097	100.0	199	10	US-09-785-738A-2
2	955.5	87.1	198	10	US-09-785-738A-4
3	862	78.6	200	10	US-09-785-738A-12
4	812	74.0	196	10	US-09-785-738A-6
5	779	71.0	200	10	US-09-785-738A-10
6	691	63.0	189	10	US-09-785-738A-8
7	609	55.3	179	10	US-09-785-738A-16
8	586	53.4	179	10	US-09-840-787-28
9	586	53.4	206	10	US-09-925-301-1387
10	581.5	53.0	181	10	US-09-785-738A-18
11	539.5	49.2	187	10	US-09-785-738A-14
12	129	11.8	181	10	US-09-815-242-5091
13	121.5	11.1	180	10	US-09-815-242-11693
14	95	8.7	153	10	US-09-867-550-458
15	84	7.7	333	10	US-09-971-791-6
16	81	7.4	313	10	US-09-971-791-8
17	81	7.4	313	10	US-09-971-791-9
18	78	7.1	287	10	US-09-912-787-4
19	78	7.1	287	10	US-09-912-787-57

20	78	7.1	287	12	US-10-014-326-43	Sequence 43, Appl
21	78	7.1	287	12	US-10-014-326-68	Sequence 68, Appl
22	78	7.1	305	10	US-09-912-787-6	Sequence 6, Appl
23	78	7.1	305	12	US-10-014-326-70	Sequence 70, Appl
24	78	7.1	497	9	US-09-981-353-105	Sequence 105, App
25	77	7.0	313	10	US-09-971-791-7	Sequence 7, Appl
26	74.5	6.8	540	12	US-10-022-461-2	Sequence 2, Appl
27	74	6.7	803	9	US-09-968-436B-2	Sequence 2, Appl
28	74	6.7	803	10	US-09-759-010-7	Sequence 7, Appl
29	70.5	6.4	302	10	US-09-815-242-5495	Sequence 5495, Ap
30	70.5	6.4	312	10	US-09-815-242-12432	Sequence 12432, A
31	70	6.4	316	10	US-09-462-846-5	Sequence 5, Appl
32	70	6.4	1534	9	US-09-736-968A-10	Sequence 10, Appl
33	70	6.4	1534	10	US-09-736-969A-10	Sequence 10, Appl
34	70	6.4	1534	10	US-09-736-960-10	Sequence 10, Appl
35	69.5	6.3	4861	10	US-09-919-497-70	Sequence 70, Appl
36	69	6.3	696	10	US-09-815-242-5443	Sequence 5443, Ap
37	69	6.3	698	10	US-09-815-242-12325	Sequence 12325, A
38	68.5	6.2	544	10	US-09-887-389-2	Sequence 2, Appl
39	68	6.2	539	10	US-09-965-313-6	Sequence 6, Appl
40	67.5	6.2	668	10	US-09-925-300-1677	Sequence 1677, Ap
41	67	6.1	357	10	US-09-907-537-2	Sequence 2, Appl
42	67	6.1	498	10	US-09-815-242-10556	Sequence 10556, A
43	67	6.1	500	10	US-09-815-242-5007	Sequence 5007, Ap
44	66.5	6.1	145	10	US-09-864-761-44376	Sequence 44376, A
45	66.5	6.1	200	10	US-09-966-608-7	Sequence 7, Appl

ALIGNMENTS

RESULT 1
US-09-785-738A-2
; Sequence 2, Application US/09785738A
; Patent No. US20020032918A1
; GENERAL INFORMATION:
; APPLICANT: Sauter, Margaret M
; APPLICANT: Lotbuecke, Rene
; TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
; FILE REFERENCE: 2283/201
; CURRENT APPLICATION NUMBER: US/09/785,738A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,572
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 199
; TYPE: PRT
; ORGANISM: Rice
US-09-785-738A-2

Query Match	100.0%	Score	1097	DB	10	Length	199
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Matches	199	Conservative	0	Matches	0	Gaps	0
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Db	1	MENEFDGKTEVIAWYMDSEEDQRLPHHREPKEFPVDKLTGVLISWRLNPDNWC	60				
QY	61	ENLKRIRARGSYVDCVCPKLPNYETKIKSPFEEHLHTDEIRYCLEGGYFVD	120				
Db	61	ENLKRIRARGSYVDCVCPKLPNYETKIKSPFEEHLHTDEIRYCLEGGYFVD	120				
QY	121	QNDQWIRALKKGMIVLPAGMYHRTLDNDYIKAMRLFVGDPVWTPYNRPHDLK	180				
Db	121	QNDQWIRALKKGMIVLPAGMYHRTLDNDYIKAMRLFVGDPVWTPYNRPHDLK	180				
QY	181	EFLAKLLKSEGENOAVEGF	199				
Db	181	EFLAKLLKSEGENOAVEGF	199				

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RESULT 2
US-09-785-738A-4
; Sequence 4, Application US/09785738A
; Patent No. US20020032918A1
GENERAL INFORMATION:
APPLICANT: Sauter, Margaret M
APPLICANT: Lorbiecke, Rene
TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 2283/201
CURRENT APPLICATION NUMBER: US/09785,738A
CURRENT FILING DATE: 2001-02-16
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 4
LENGTH: 198
TYPE: PRT
ORGANISM: Rice
-09-785-738A-4

Query Match      87.1%; Score 955.5; DB 10; Length 198;
Best Local Similarity 85.3%; Pred. No. 5.1e-88;
Matches 168; Conservative 19; Mismatches 9; Indels 1; Gaps 1;

1 MENEFODGTEVIEAWYMDSDSDORLPHHREKPEFIPVDKLTGELGVISWRINPNWENC 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
1 MENOFQDGEVIEAWYMDSDSDORLPHHREKPEFIPVDKLTGELGVISWRINPNWENC 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
61 ENLKRIEARGYSYVDICDVCPEKLPNYETKIKSFEEHLHTDEEIRYCLSGSYFVDVRD 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
61 ENLKRIEARGYSYMDICDVCPEKLPNYEAKLNKFFEEHLHTDEEIRYCLSGSYFVDVRD 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
121 QNDQWIRIALKGGMIVLPAGMYHRTLDTONYIKAMRLFVGDVPVWTPYNNRPHDLHPARK 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
121 QNDQWIRVAVKGGMIVLPAGMYHRTLDTONYIKAMRLFVGDVPVWTPYNNRPHDLHPARK 180
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
181 EFLAKLKSEGENQAVE 197
||: ||: | ||||
181 EYVEKII-NRGSTQAVE 196
||: ||: | ||||

LT 3
9-785-738A-12
; Sequence 12, Application US/09785738A
; Patent No. US20020032918A1
GENERAL INFORMATION:
APPLICANT: Sauter, Margaret M
APPLICANT: Lorbiecke, Rene
TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 2283/201
CURRENT APPLICATION NUMBER: US/09785,738A
CURRENT FILING DATE: 2001-02-16
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.1
SEQ ID NO 12
LENGTH: 200
TYPE: PRT
ORGANISM: Cotton
785-738A-12

Y Match      78.6%; Score 862; DB 10; Length 200;
Local Similarity 77.5%; Pred. No. 1.1e-78;
Matches 148; Conservative 24; Mismatches 19; Indels 0; Gaps 0;

7 DGKTEVIAWYMDSDSDORLPHHREKPEFIPVDKLTGELGVISWRINPNWENCENLKRI 66
||: ||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
7 DKREVIQAWYMDSDSDORLPHHREKPEYVSLDKLAELGVLSRLDADNYETDELKKI 66
||: ||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||

Query Match      74.0%; Score 812; DB 10; Length 196;
Best Local Similarity 73.2%; Pred. No. 9.7e-74;
Matches 139; Conservative 28; Mismatches 23; Indels 0; Gaps 0;

QY 7 DGKTEVIAWYMDSDSDORLPHHREKPEFIPVDKLTGELGVISWRINPNWENCENLKRI 66
||: ||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
DB 3 DPREDVIQAWYMDSDSDORLPHHREKPEVSLDKLAELGVLSRLDADNYETDELKKI 62
||: ||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||

QY 67 REARGYSYVDICDVCPEKLPNYETKIKSFEEHLHTDEEIRYCLSGSYFVDVRDNDOWI 126
|| ||||| ||: ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||
DB 63 REDRGYSYIDFCEVCPEKLPNYEIKNFEEHLHTDEEIRYAVAGSGYFVDVRDNESWI 122
||: ||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||

QY 127 RIALKGGMIVLPAGMYHRTLDTONYIKAMRLFVGDVPVWTPYNNRPHDLHPARKEFLAKL 186
||: ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||
DB 123 RYVVKGGMIVLPAGIYHRTLDSSNYIKAMRLFVGDPIWTYPYNNRPHDLHPARQYIVETF 182
||: ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||

QY 187 LKSEGENQAV 196
||: ||: |||
DB 183 VNADGAGRAV 192
||: ||: |||

RESULT 5
US-09-785-738A-10
; Sequence 10, Application US/09785738A
; Patent No. US20020032918A1
GENERAL INFORMATION:
APPLICANT: Sauter, Margaret M
APPLICANT: Lorbiecke, Rene
TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
TITLE OF INVENTION: CONDITIONS
FILE REFERENCE: 2283/201
CURRENT APPLICATION NUMBER: US/09785,738A
CURRENT FILING DATE: 2001-02-16
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patent In Ver. 2.1
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; TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
; FILE REFERENCE: 2283/201
; CURRENT APPLICATION NUMBER: US/09/785,738A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,572
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 179
; TYPE: PRT
; ORGANISM: Mouse
; ORIGIN: 785-738A-16
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Query Match          55.5%; Score 609; DB 10; Length 179;
Best Local Similarity 60.0%; Pred. No. 1.4e-53;
Matches 105; Conservative 32; Mismatches 38; Indels 0; Gaps 0;
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QY 12 VIEAWYMDDEEDORLPHRRPEKFIYVDKLTGLGVISWRLNPNWNCENLARIREARG 71
DB 1 MVQAWYMDDESTADPRKPRHAPDPSVDEQLRTGLVLYWKLDADYNDPELEKIRKRN 60
QY 72 YSYVDICDVCEKPLPNYETKIKSFEEHLHTDEEIRYCLESGYFVDVNDQWIRIALK 131
DB 61 YSWMDIITICKDPLNPEYEEKIKMFEEHLHLDDEEIRYLESGYFVDVREDKWIIRISME 120
QY 132 KGGMIVLPACMYHREFTLDNTYIKAMRLFYGDVPVTPYNNRPHDLPAKKEFLAKL 186
DB 121 KGDMITLPAGIYHREFTLDEKNYKAMRLFYGDVPVTPYNNRPAHDFDARVOYMSFL 175
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RESULT B
; US-09-840-787-28
; Sequence 28, Application US/09840787
; Patent No. US20020058264A1
; GENERAL INFORMATION:
; APPLICANT: Lal, Preeti
; Hillman, Jennifer L.
; Bandman, Olga
; Shah, Purvi
; Au-Young, Janice
; Yue, Henry
; Guegler, Karl J.
; Corley, Neil C.
;
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSER: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
;
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/840,787
FILING DATE: 23-Apr-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/518,865
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166

```

TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
LENGTH: 179 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LMODNOT03
CLONE: 1577239
SEQUENCE DESCRIPTION: SEQ ID NO: 28 :
US-09-840-787-28

Query Match 53.4%; Score 586; DB 10; Length 179;
Best Local Similarity 56.7%; Pred. No. 2.7e-51;
Matches 101; Conservative 34; Mismatches 43; Indels 0; Gaps 0;
y 12 VIEAWYMDSEEDQRLPHHREPKEFIPVDKLTGELVSWLNPNDWNCENLKRIEARG 71
b 1 MVQAWYMDADGDPQHPDPGRPVGLEQLRLGLVYKLDADKYENDPELEKIRERN 60
y 72 YSYVDICDVCPEKLPNYETKISFEEHLHTDEIRYCLEGSGYFVDRDQNDQWIRIALK 131
b 61 YSWMDIITICKDKLPNYEETKIMFYEEHLHLDDEIRYILDGSGYFVDRDQNDQWIRIFME 120
y 132 KGMIVLPAGMYHREFTLTDNYIKAMRLFVGPVWTPYRNPHDHLPAKKEFLAKLKS 189
b 121 KGMVTLPAIGYHREFTVDEKNTKAMRLFVGPVWTPYRNPHDHLPAKKEFLAKLKS 178

SULT 9

-09-925-301-1387
Sequence 1387, Application US/09925301
Patent No. US20020032918A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925,301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: PatentIn Ver. 2.0
Q ID NO 1387
LENGTH: 206
TYPE: PRT
ORGANISM: Homo sapiens
US-925-301-1387

ry Match 53.4%; Score 586; DB 10; Length 206;
t Local Similarity 56.7%; Pred. No. 3.3e-51;
ches 101; Conservative 34; Mismatches 43; Indels 0; Gaps 0;
12 VIEAWYMDSEEDQRLPHHREPKEFIPVDKLTGELVSWLNPNDWNCENLKRIEARG 71
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72 YSYVDICDVCPEKLPNYETKISFEEHLHTDEIRYCLEGSGYFVDRDQNDQWIRIALK 131
88 YSWMDIITICKDKLPNYEETKIMFYEEHLHLDDEIRYILDGSGYFVDRDQNDQWIRIFME 147
132 KGMIVLPAGMYHREFTLTDNYIKAMRLFVGPVWTPYRNPHDHLPAKKEFLAKLKS 189
148 KGMVTLPAIGYHREFTVDEKNTKAMRLFVGPVWTPYRNPHDHLPAKKEFLAKLKS 205

10
85-738A-18
nce 18, Application US/09785738A
t No. US20020032918A1

GENERAL INFORMATION:
APPLICANT: Sauter, Margret M
APPLICANT: Lorbiecke, Rene
TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
CONDITIONS
FILE REFERENCE: 2283/201
CURRENT APPLICATION NUMBER: US/09/785,738A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,572
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 181
TYPE: PRT
ORGANISM: zebrafish
OTHER INFORMATION: n at positions 634 and 642 is unknown
US-09-785-738A-18

Query Match 53.0%; Score 581.5; DB 10; Length 181;
Best Local Similarity 55.1%; Pred. No. 7.8e-51;
Matches 104; Conservative 28; Mismatches 43; Indels 1; Gaps 1;
Qy 12 VIEAWYMD-0SEEDQRLPHHREPKEFIPVDKLTGELVSWLNPNDWNCENLKRIEARG 70
Db 3 VFEAWYMDSEEDQRLPHKLSNPQPVSVQQLGHEIGVPHKLNADYENDPELEKIREEK 62
Qy 71 GYSYVDICDVCPEKLPNYETKISFEEHLHTDEIRYCLEGSGYFVDRDQNDQWIRIAL 130
Db 63 GYSFMDIITIHDPKLPDYQNKLMFYEEHLHLDDEIRYILEGSGYFVDRDQNDQWIRIAV 122
Qy 131 KKGSMIVLPAGMYHREFTLTDNYIKAMRLFVGPVWTPYRNPHDHLPAKKEFLAKL 186
Db 123 SKGDLITLPAGIYHREFTVDESNYTKAMRLFVGPVWTPYRNPHDHLPAKKEFLAKL 178

RESULT 11

US-09-785-738A-14
Sequence 14, Application US/09785738A
Patent No. US20020032918A1
GENERAL INFORMATION:
APPLICANT: Sauter, Margret M
APPLICANT: Lorbiecke, Rene
TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
CONDITIONS
FILE REFERENCE: 2283/201
CURRENT APPLICATION NUMBER: US/09/785,738A
CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: 60/183,572
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 187
TYPE: PRT
ORGANISM: Human
US-09-785-738A-14

Query Match 49.2%; Score 539.5; DB 10; Length 187;
Best Local Similarity 55.1%; Pred. No. 1.2e-46;
Matches 98; Conservative 29; Mismatches 50; Indels 1; Gaps 1;
Qy 12 VIEAWYMDSEEDQRLPHHREPKEFIPVDKLTGELVSWLNPNDWNCENLKRIEARG 71
Db 10 VQAWYMDADGDPQHPDPGRPVGLEQLRLGLVYKLDADKYENDPELEKIRERN 68
Qy 72 YSYVDICDVCPEKLPNYETKISFEEHLHTDEIRYCLEGSGYFVDRDQNDQWIRIALK 131
Db 69 YSWMDIITICKDKLPNYEETKIMFYEEHLHLDDEIRYILDGSGYFVDRDQNDQWIRIFME 128
Qy 132 KGMIVLPAGMYHREFTLTDNYIKAMRLFVGPVWTPYRNPHDHLPAKKEFLAKL 186
Db 179 KGMVTLPAIGYHREFTVDESNYTKAMRLFVGPVWTPYRNPHDHLPAKKEFLAKL 178

Query Match 8.78; Score 95; DB 10; Length 153;

```

Best Local Similarity 25.9%; Pred. No. 0.017;
Matches 37; Conservative 20; Mismatches 64; Indels 22; Gaps 5;

QY 28 PHHREKPEFIPVDKLTGLGVISWR-----LNPDNWCENLKRIRAE-----RGYS 73
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 14 PELASNDPDVIASRLREIGVRFERWASPVALSFD-----DPAETILEAYRPHLDALMGES 68
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 74 YVDICDV--CPEKLPNYETKIKSFEEHLHTDEIRYCYCLEGSGYFDVRDQNDQWIRIALK 131
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 69 GAGSADVIKISAATPNKQALDKFLSEHQHTEDEVRFVHGSGNF--IHVYDGRVDAHCT 127
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 KGMIVILPAGMYKHFYLTDTDNVI 154
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB 128 QGDLSIVPEASTKHWFADAGDPFV 150
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
IS-09-971-791-6
Sequence 6, Application US/09971791
Patent No. US20020115120A1
GENERAL INFORMATION:
APPLICANT: Rosanna Kapeller-Libermann
APPLICANT: Laura A. Rudolph-Owen
APPLICANT: Kyle MacBach
TITLE OF INVENTION: NOVEL MOLECULES OF THE HKID-1-RELATED PROTEIN FAMILY AND USES THEREOF
FILE REFERENCE: 35800/2338856
CURRENT APPLICATION NUMBER: US/09/971,791
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/644,450
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: 09/237,543
PRIOR FILING DATE: 1999-01-26
NUMBER OF SEQ ID NOS: 11
SOFTWARE: FastSeq for Windows Version 4.0
>EO ID NO 6
LENGTH: 323
TYPE: PRT
ORGANISM: Xenopus laevis
09-971-791-6

very Match 7.7%; Score 84; DB 10; Length 323;
Best Local Similarity 24.2%; Pred. No. 0.55;
Matches 37; Conservative 27; Mismatches 57; Indels 32; Gaps 9;

33 KPEFIPVDKLT-----LQVISWRNLNDNN-----ENCNLKRIRAEARGYSYVDICDVCE 83
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
88 PLEIVLLKKPYTAFRGVINLDWYERDPAFLIVMERPEVK-----DLFDYITE 136
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
84 KLPNYETKIKSFEEHLHTDEIRYCYCLE--GSGYFDVRDQNDQWIRIALKKG--GMIVLEA 140
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
137 KGPLDQETAGRFQVQL---EAVRHCTNCGVWVHRDKDEN---LLVDTRNGELKLIIDFGS 190
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
141 GMVHRTFLTDNYIKAMRLFVGDVPVTFYMRPH 173
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :
191 GALLKDTVYTD--FDGTRYV--SPPEWVRYHRYH 220
      : : : : : : : : : : : : : : : : : : : : : : : : : : : :

h completed: November 25, 2002, 10:13:50
Time : 11 secs

```

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

protein search, using sw model

November 25, 2002, 10:08:00 ; Search time 20 Seconds
(without alignments)
956,537 Million cell updates/sec

score: 1097
1 MENEFDQKTEVTEAMDD.....KEFLAKLLKSEGENQAVEGF 199

table: BLOSUM62
Gapop 10.0 , Gapext 0.5

l: 283224 seqs, 96134422 residues
number of hits satisfying chosen parameters: 283224

DB seq length: 0
DB seq length: 2000000000
processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

se: PIR 73:3
1: PIR1:
2: PIR2:
3: PIR3:
4: PIR4:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

s.	t	Score	Query Match	Length	DB	ID	Description
1	1097	100.0	199	2	T02787		probable submergen
2	955.5	87.1	198	2	T02918		probable submergen
3	789.5	72.0	940	2	H71409		hypothetical prote
4	781	71.2	199	2	T00973		hypothetical prote
5	362	33.0	179	2	S53039		probable nickel-bi
6	307.5	28.0	178	2	T40726		probable nickel-bi
7	307.5	28.0	178	2	T22103		hypothetical prote
8	229	20.9	221	2	T16578		hypothetical prote
9	227	20.7	159	2	T29472		hypothetical prote
10	192	17.5	178	2	B69884		probable methionin
11	148	13.5	188	2	F82587		dioxygenase XF2210
12	138	12.6	183	2	E70469		probable methionin
13	129	11.8	181	2	E83436		probable oxidase P
14	121.5	11.1	182	2	A62146		hypothetical prote
15	118	10.8	180	1	A59159		methionine salvage
16	91	8.3	399	2	B70349		hypothetical prote
17	90	8.2	659	2	A75029		h+-transporting AR
18	87.5	8.0	307	2	A42902		transcription regu
19	87.5	8.0	307	2	F83198		transcription regu
20	86.5	7.9	264	2	S49787		hypothetical prote
21	85.5	7.9	465	2	H86482		protein F5J5.11 [i
22	85.5	7.8	286	2	A84070		3-hydroxyanthranil
23	85.5	7.8	315	2	D84139		mannose-6-phosphat
24	85.5	7.8	1279	2	E84709		type IIS restricti
25	83.5	7.6	4273	2	C89679		polyketide synthas
26	82	7.5	518	1	FWOAG1		12S seed storage g
27	81.5	7.4	136	2	C97153		probable transcrip
28	81.5	7.4	337	2	F70323		transcription term
29	81	7.4	313	1	TVHUP1		protein kinase (EC

30 81 7.4 313 1 S26298
31 81 7.4 508 2 S35692
32 80.5 7.3 502 2 S35158
33 80.5 7.3 514 2 T39458
34 80 7.3 360 1 S41759
35 80 7.3 311 2 D97058
36 80 7.3 493 2 S17762
37 80 7.3 795 2 S33101
38 80 7.3 795 2 T28525
39 80 7.3 795 2 E72161
40 79.5 7.2 709 2 S40926
41 79.5 7.2 784 2 C88558
42 79.5 7.2 1471 1 S30790
43 79 7.2 575 1 QOVZHS
44 79 7.2 714 2 T22454
45 79 7.2 795 1 QOVZHS

ALIGNMENTS

RESULT 1

T02787
probable submergence induced protein 2 - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999
C:Accession: T02787
R:Lorbiecke, R.; Sauter, M.
submitted to the EMBL Data Library, February 1998
A:Reference number: Z14738
A:Accession: T02787
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-199 <LOR>
A:Cross-references: EMBL:AF050200; NID:g2952337; PID:g2952338
C:Genetics:
A:Gene: SIP2

Query Match 100.0%; Score 1097; DB 2; Length 199;
Best Local Similarity 100.0%; Pred. No. 6e-88;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MENEFDQKTEVTEAMDDSEEDQRLPHRPEKEFIPVDKLTGLGVISMRKLPNDWNC 60

Db 1 MENEFDQKTEVTEAMDDSEEDQRLPHRPEKEFIPVDKLTGLGVISMRKLPNDWNC 60

Qy 61 ENLKRIEARGSYVDICDVCPEKLPNYETKIKSFEEHLHTDEIRYCLESGYFDVRD 120

Db 61 ENLKRIEARGSYVDICDVCPEKLPNYETKIKSFEEHLHTDEIRYCLESGYFDVRD 120

Qy 121 QNDQWIRIALKKGGMIVLPACMYHRTLDTDNYIKAMRLFVGDVPTPNRPHDLPAK 180

Db 121 QNDQWIRIALKKGGMIVLPACMYHRTLDTDNYIKAMRLFVGDVPTPNRPHDLPAK 180

Qy 181 EFLAKLLKSEGENQAVEGF 199

Db 181 EFLAKLLKSEGENQAVEGF 199

RESULT 2

T02918
probable submergence induced, nickel-binding protein 2A - rice
C:Species: Oryza sativa (rice)
C:Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
C:Accession: T02918
R:Lorbiecke, R.; Sauter, M.
submitted to the EMBL Data Library, May 1998
A:Reference number: Z14768
A:Accession: T02918
A:Status: preliminary; translated from GB/EMBL/DBBJ
A:Molecule type: mRNA
A:Residues: 1-196 <LOR>
A:Cross-references: EMBL:AF068332; NID:g3201968; PID:g3201969

C:Keywords: metalloprotein: nickel
F:98.99,101.144/Binding site: nickel (Glu, His, His) #status predicted

Query Match 87.1%; Score 955.5; DB 2: Length 198;
Best Local Similarity 85.3%; Pred. No. 1.1e-75;

Matches 166; Conservative 19; Mismatches 9; Indels 1; Gaps 1;

QY 1 MENEFQDGKTEVTEAWYMDSEEDQRLPHHREKPEIPVDKLTGLGVISWLNPDWNC 60

Db 1 MENEFQDGKTEVTEAWYMDSEEDQRLPHHREKPEIPVDKLTGLGVISWLNPDWNC 60

QY 61 ENLKRIRREAGSYVDICDVCPEKLPNYETKIKSFEEHLHTDEEIRYCLGSGYDVRD 120

Db 61 ENLKRIRREAGSYVDICDVCPEKLPNYETKIKSFEEHLHTDEEIRYCLGSGYDVRD 120

QY 121 QNDQWIRIALKKGCMIVLPAGMYHRTLDYNIKAMRLFGVDPVWTPYRPHDHLPAK 180

Db 121 QNDQWIRIALKKGCMIVLPAGMYHRTLDYNIKAMRLFGVDPVWTPYRPHDHLPAK 180

QY 181 EFLAKLKSEGNQAVE 197

Db 181 EFLAKLKSEGNQAVE 197

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

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Db 181 EYVEKII-NRGQTQAVE 196

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Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 23-Mar-2001

C:Accession: T00973; A84660
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; K

submitted to the EMBL data library, April 1998
A:Description: Arabidopsis thaliana chromosome II BAC T9J22 genomic sequence.

A:Reference number: Z14161
A:Accession: T00973

A:Status: translated from GB/EMBL/DDAJ
A:Molecule type: DNA

A:Residues: 1-199 <ROU>
A:Cross-references: EMBL:AC002505; NID:g2739359; PID:g2739365

A:Experimental source: cultivar Columbia
A:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, J.

ess, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: A84660

A:Status: preliminary
A:Molecule type: DNA

A:Residues: 1-199 <STO>
A:Cross-references: GB:AE002093; NID:g2739365; PIDN:AA014490.1; GSPDB:GN00139

C:Genetics:
A:Gene: At2g26400; T9J22.7

A:Map position: 2
A:Introns: 6/3; 44/1; 75/3; 114/1; 155/3; 179/2

Query Match 71.2%; Score 781; DB 2: Length 199;
Best Local Similarity 71.7%; Pred. No. 1.6e-60;

Matches 134; Conservative 27; Mismatches 26; Indels 0; Gaps 0;

QY 6 QDCKTEVIAWYMDSEEDQRLPHHREKPEIPVDKLTGLGVISWLNPDWNCENLAK 65

Db 6 QDCKTEVIAWYMDSEEDQRLPHHREKPEIPVDKLTGLGVISWLNPDWNCENLAK 65

QY 56 IREAGSYVDICDVCPEKLPNYETKIKSFEEHLHTDEEIRYCLGSGYDVRDNDOW 125

Db 56 IREAGSYVDICDVCPEKLPNYETKIKSFEEHLHTDEEIRYCLGSGYDVRDNDOW 125

QY 126 IRTALKKGMIVLPAGMYHRTLDYNIKAMRLFGVDPVWTPYRPHDHLPAKSFELAK 185

Db 126 IRTALKKGMIVLPAGMYHRTLDYNIKAMRLFGVDPVWTPYRPHDHLPAKSFELAK 185

QY 186 LKSEGE 192

Db 186 LKSEGE 192

QY 186 FLKVIQD 192

Db 186 FLKVIQD 192

QY 186 FLKVIQD 192

Db 186 FLKVIQD 192

QY 186 FLKVIQD 192

Db 186 FLKVIQD 192

QY 186 FLKVIQD 192

Db 186 FLKVIQD 192

QY 186 FLKVIQD 192

Db 186 FLKVIQD 192

QY 186 FLKVIQD 192

Db 186 FLKVIQD 192

QY 186 FLKVIQD 192

Db 186 FLKVIQD 192

QY 186 FLKVIQD 192

Db 186 FLKVIQD 192

C:Keywords: metalloprotein: nickel
F:98.99,101.144/Binding site: nickel (Glu, His, His) #status predicted

Query Match 87.1%; Score 955.5; DB 2: Length 198;
Best Local Similarity 85.3%; Pred. No. 1.1e-75;

Matches 166; Conservative 19; Mismatches 9; Indels 1; Gaps 1;

QY 1 MENEFQDGKTEVTEAWYMDSEEDQRLPHHREKPEIPVDKLTGLGVISWLNPDWNC 60

Db 1 MENEFQDGKTEVTEAWYMDSEEDQRLPHHREKPEIPVDKLTGLGVISWLNPDWNC 60

QY 61 ENLKRIRREAGSYVDICDVCPEKLPNYETKIKSFEEHLHTDEEIRYCLGSGYDVRD 120

Db 61 ENLKRIRREAGSYVDICDVCPEKLPNYETKIKSFEEHLHTDEEIRYCLGSGYDVRD 120

QY 121 QNDQWIRIALKKGCMIVLPAGMYHRTLDYNIKAMRLFGVDPVWTPYRPHDHLPAK 180

Db 121 QNDQWIRIALKKGCMIVLPAGMYHRTLDYNIKAMRLFGVDPVWTPYRPHDHLPAK 180

QY 181 EFLAKLKSEGNQAVE 197

Db 181 EFLAKLKSEGNQAVE 197

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

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Db 181 EYVEKII-NRGQTQAVE 196

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Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

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QY 181 EYVEKII-NRGQTQAVE 196

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QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196

QY 181 EYVEKII-NRGQTQAVE 196

Db 181 EYVEKII-NRGQTQAVE 196


```

Query Match      28.0%: Score 307.5; DB 2: Length 178;
Best Local Similarity 34.4%: Pred No. 1.8e-19;
Matches 63; Conservative 37; Mismatches 66; Indels 17; Gaps 2;

QY 15 AWYWDSEDDORLPHHR-EPKEFIPVDKLTTELGVISWRNLNPDNWNCENLKRRTEARGYS 73
DB 2 AIFWIDVTENKQDCRSPKNEATEGDLRIIGVCTKVFNDDEHVDDLDLRIKYDMN 61
QY 74 YVDCIDVCPEKLPNYETIKKSPFBEHLHTDEIRYCLESGSYFVDVRDNDQWIRIALKKG 133
DB 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
62 FHDEVHICRATPNFDEKLDLFFEHHLDDAELRVIKHGCVGFVDVYRKDEAMIRIPVRG 121
QY 134 GMIVLPAGMYHRETTLDITNYIKAMRLEVGDPVWTPYNRPHDLHPARKEFLAKLLKSEGN 193
DB 1 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
122 DFVEFAGIYHRETTDPSEDVVALRLFRNPKVTAENR-----KADGDE 165
QY 194 QAV 196
DB 1 : :
166 QRV 168

RESULT 8
T16578
hypotheical protein K07EI.1 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999
C:Accession: T16578
R:Fulton, B.
submitted to the EMBL Data Library, July 1995
A:Description: The sequence of C. elegans cosmid K07EI.
A:Reference number: Z18539
A:Accession: T16578
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-221 <PUL>
A:Cross-references: EMBL:U23173; NID:G736396; PID:G726397; PIDN:AAC46708.1;
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:K07EI.1
A:Introns: 15/3; 206/3

Query Match      20.9%: Score 229; DB 2: Length 221;
Best Local Similarity 33.1%: Pred No. 1.5e-12;
Matches 53; Conservative 33; Mismatches 70; Indels 4; Gaps 4;

QY 7 DCKTEVTANYMDSE-EDORLPHPREKPEIPVDKLTE-LGVISWRNLNP-DWNEENL 63
DB 59 DFQUKWVOIWMQPEYPCGDPRLPHLPFPKIPDPDELSRGTGLTWKLTLOQVALAKRL 118
QY 64 KRIAREAGYSYDVICDVCPEKLPNYETIKKSPFBEHLHTDEIRYCLESGSYFVDVRDND 123
DB 119 TTLKLEHSFKKEDIFTLDAETANFDDKIEELFEESVVPFEQARMIIETGATYDVEDKNG 178
QY 124 QWIRIALKKGMIVLPAAGMYHRETTLDITNYIKAMRLEFVG 163
DB 179 QWVRFCEYGDILIPANTCFRETTTPHNFVK-MRREYKD 217

RESULT 9
T29472
hypotheical protein T01D1.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C:Accession: T29472
R:Bradshaw, H.; Wohlmann, P.
submitted to the EMBL Data Library, November 1996
A:Description: The sequence of C. elegans cosmid T01D1.
A:Reference number: Z20623
A:Accession: T29472
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-159 <BRA>

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RESULT 2	
Y545_AQUAE	
ID Y545_AQUAE	STANDARD;
AC O65822;	PRT; 399 AA.

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EMBL; M84911; AAA25890.1; -.
EMBL; AE004778; AAG06959.1; -.
PIR; S27601; S27601.
PIR; A42902; A42902.
InterPro; IPR000005; HTHArac.
Pfam; PF00165; HTH_Arac; 2.
PRINTS; PR00032; HTHARAC.
SMART; SM00342; HTH_ARAC; 1.
PROSITE; PS00041; HTH_ARAC_FAMILY_1; 1.
PROSITE; PS01124; HTH_ARAC_FAMILY_2; 1.
Transcription regulation; DNA-binding; Activator; Complete proteome.
DNA_BIND 217 236 H-T-H MOTIF (BY SIMILARITY).
CONFLICT 129 129 S -> T (IN REF. 1).
SEQUENCE 307 AA; 35379 MW; 9BF7AEE348FAFD45 CRC64;

```

ry Match      8.0%; Score 87.5; DB 1; Length 307;
Local Similarity 28.2%; Pred. No. 1.8;
ches 20; Conservative 10; Mismatches 40; Indels 1; Gaps 1;

79 DVCPEKLPWYTKIKSFEEHLHTDDEIRYRCLEGSGYDVRDQNDQMIALKKGGMVL 138
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
44 DLYTSLGHYRRAROHRRMSRERHDEHLLIYCSEGGLLRVR-EGEAWREYRVGSGDLLWL 102
   | : | : | : | : | : | : | : | : | : | : | : | : | : | : |

139 PAGMYHREFTLD 149
   | | | | | : |
103 PPGMAHDYAAD 113

```

T 5
YEAST
YIJ3_YEAST
P40496;
STANDARD; PRT; 264 AA.
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
Hypothetical 30.5 kDa protein in SG1-KTR7 intergenic region.
Y1L093C.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI TaxID:4932;

SEQUENCE FROM N.A.
STRAIN-5288C / AB972:
Barrell B.G., Badcock
Churcher C.M., Connor R., Copsey T., Dear S., Devlin K., Fraser A.,
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones M.,
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rejzbrand M.A., Riles N., Rowley N., Skelton J., Smith V.,
Walsh S.V., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.

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or send an email to license@isb-sib.ch).

EMBL: Z45728; CAA86701.1; -.
SGD: S0001355; YIL093C.
Hypothetical protein.
SEQUENCE 264 AA; 30513 MW; D6E5BB8B1A2B6C2E CRC64;

```

Query Match      7.9%; Score 86.5; DB 1; Length 264;
Best Local Similarity 23.2%; Pred. No. 1.9;
Matches 48; Conservative 29; Mismatches 75; Indels 55; Gaps 11;

      QY      6 QDCKTEVIEAWY-----MDSIEDQRLLPHREKEFPVDKLTLEL-----GVISWR 51
      DB      19 KSGLLKETPAWYNVASIPSTKFTREPRKFNPSNGHIIGKLVDTQEPHANNKGLYKTR 78

      QY      52 LNPDNWENCNLRKRIRREARYSYVDICDVCPEKLPNVTIKS--FFEHUHTDDEIRYCL 110
      DB      79 PNSSD-----KRVGVKRLYR-----PPKLTYYVEDRLSLFYKQHPWELSRPKLY 123

      QY      111 EGSGYFDVRDQNDQW---IRIALKGGMIVLPAGMYHREFTLDTDNYIKAMRLFVGDPPWVT 167
      DB      124 EN---EIGDENYDWSHMLQIGRPDGESVIQRTMY---LIKTQY-----GDMV-- 166

      QY      168 PYNRPHDHLPARKEFLAKLKSEGENQ 194
      DB      167 ---EAYDH--ARYEYALRMOEETEQQ 188

```

```

RESULT 6
3HAO_HUMAN STANDARD; PRT; 286 AA.
ID 3HAO_HUMAN STANDARD; PRT; 286 AA.
P46952;
AC DT 01-NOV-1995 (Rel. 32, Created)
AC DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE DE 3-hydroxyanthranilate 3,4-dioxygenase (EC 1.13.11.6) (3-HAO)
DE DE (3-hydroxyanthranilic acid dioxygenase) (3-hydroxyanthranilate
DE DE dioxygenase).
DE HA00.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_TaxId=9606;
OX [1]
SEQUENCE FROM N.A.
MEDLINE=94245687; PubMed=7514594;
RX Malherbe P., Kohler C., da Prada M., Lang G., Kiefer V.,
RA Schwarcz R., Lahm H., Cesura A.M.;
RT "Molecular cloning and functional expression of human 3-
RT hydroxyanthranilic acid dioxygenase.";
RL J. Biol. Chem. 269:13792-13797(1994).
CC CC -!- FUNCTION: CATALYZES THE SYNTHESIS OF THE EXCITOPOXIN QUINOLINIC
CC CC ACID (QUIN) FROM 3-HYDROXYANTHRANILIC ACID. THE DIRECT PRODUCT
CC CC OF THE REACTION SPONTANEOUSLY REARRANGE TO QUIN.
CC CC -!- CATALYTIC ACTIVITY: 3-hydroxyanthranilate + O(2) -> 2-amino-3-
CC CC carboxymuconate semialdehyde.
CC CC -!- COFACTOR: FERROUS ION.
CC CC -!- SUBUNIT: MONOMER.
CC CC -!- SUBCELLULAR LOCATION: Cytoplasmic.
CC CC
CC CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC CC entities requires a license agreement (See http://www.isb-sib.ch/announcement/
CC CC or send an email to license@isb-sib.ch).
CC CC
CC CC EMBL; Z29481; CAA82618.1; --
CC CC Genew; HGNC:4796; HAA0.
CC CC MIM; 604521; --
CC CC Oxidoreductase; Dioxygenase; Iron.
CC CC SEQUENCE 286 AA; 32542 MW; 4DA10F20FC635885 CRC64;
SQ

```

```
Query Match          7.8%; Score 85.5; DB 1; Length 286;  
Best Local Similarity 24.1%; Pred. No. 2.5;  
Matches 34; Conservative 25; Mismatches 37; Indels 45; gaps 7;  
  
QY    45 LGVISRLPNPDNWCENLKRIRREARYSYVDICDVCPEKLPNYETRIKSF----- 96  
      ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
```


[illegible]

```
Subtilist: BG10931; pkms.
InterPro: IPR002198; ADH_short.
InterPro: IPR000794; Ketoacyl-synt.
InterPro: IPR001601; Methyltransf.
InterPro: IPR003880; Plantne_attach.
InterPro: IPR000051; SAM_bind.
Pfam: PF00106; adh_short; 1.
Pfam: PF00109; ketoacyl-synt; 3.
Pfam: PF00550; pp-binding; 4.
Pfam: PF02801; ketoacyl-synt_C; 3.
PROSITE: PS00012; PHOSPHOPANTETHEINE; 2.
PROSITE: PS00606; B_KETOACYL_SYNTHASE; 2.
PROSITE: PS50075; AC-DOMAIN; 4.
Transferrase; Acyltransferase; Antibiotic biosynthesis; NADP;
Phosphopantetheine; Multifunctional enzyme; Repeat; Complete proteome.
DOMAIN 295 364
DOMAIN 396 834
DOMAIN 2190 2258
DOMAIN 2322 2737
DOMAIN 3532 3947
DOMAIN 3410 3483
DOMAIN 4140 4209
DOMAIN 327 327
BINDING 2222 2222
ACT_SITE 2476 2476
ACT_SITE 3446 3446
ACT_SITE 3690 3690
ACT_SITE 4172 4172
CONFLICT 103 103
CONFLICT 276 276
CONFLICT 289 289
SEQUENCE 4273 AA; 477459 MW; 3BBFCF1A250AEB5A CRC64;

Query Match 7.6%; Score 83.5; DB 1; Length 4273;
Best Local Similarity 22.2%; Pred. No. 74;
Matches 54; Conservative 24; Mismatches 64; Indels 101; Gaps 11;

11 EVTEAWMDSEEDQLPH-----HREP-----KEFIPVDKL 42
12 ELIEAYRDDASQAQPEAYVPALEPEASKSIRQVHDEPIAIGSGRFPQADSV 3547
43 TELGVISWRLNPDNWCENLKRI-----REARGYSY-----VDICD 79
44 ELIEAYRDDASQAQPEAYVPALEPEASKSIRQVHDEPIAIGSGRFPQADSV 3547
548 HEL-----WDNLKNGKSCISDIPGERDWDGVRANRDEKAVPRMGAFKLKIDRFED 3596
80 -----VCPEKLPNYETIKISFFEEHLHTDEEIRYCLE-GSGYFDVRDNDQWIRALKKG 134
81 PLFFQISPKAESMDPRQPIFLEEAHWTFEDAGYMGD-----RIKGSKG 3641
135 MIV-LPAGMYHRTLDTDNYIKAMRLFVGDVPVTPYNNRPHDLPARKEFLAKLKSSEN 193
3642 VYGVGEYAHLTGDTD-YINGTQ-----NATLSAR---IAYALDLKGNP 3683

194 QAV 196
3684 MAL 3686

RESULT 11
IML_BOVIN
D PML_BOVIN STANDARD; PRT; 313 AA.
C Q9N0P9;
T 15-JUN-2002 (Rel. 41, Created)
T 15-JUN-2002 (Rel. 41, Last sequence update)
T 15-JUN-2002 (Rel. 41, Last annotation update)
E Proto-oncogene serine/threonine-protein kinase pim-1 (EC 2.7.1.37).
N PIM1.
S Bos taurus (Bovine).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
C Bovidae; Bovinae; Bos.
X NCBI_TaxID=9913;
N [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=21109090; PubMed=11182156;
RA Wang Z., Petersen K., Weaver M.S., Magnuson N.S.;
RT "cDNA cloning, sequencing and characterization of bovine pim-1.";
RL Vet. Immunol. Immunopathol. 78:177-195 (2001).
CC -!- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
CC -!- PTM: Autophosphorylated (By similarity).
CC -!- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
CC PIM SUBFAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF259078; AAF67200.1; -.
CC HSP: Q63450; 1A06.
CC InterPro: IPR000719; Euk_pkinase.
CC InterPro: IPR002290; Ser_thr_pkinase.
CC Pfam: PF00069; pkinase; 1.
CC ProDom: PD000001; Euk_pkinase; 1.
CC PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
CC Transferrase; Serine/threonine-protein kinase; Proto-oncogene;
KW ATP-binding; phosphorylation.
FT DOMAIN 38 290 PROTEIN KINASE
FT BINDING 44 52 ATP (BY SIMILARITY).
FT BINDING 67 67 ATP (BY SIMILARITY).
FT ACT_SITE 167 167 BY SIMILARITY.
FT SEQUENCE 313 AA; 35629 MW; 9EF40229A847AD47 CRC64;

Query Match 7.6%; Score 83; DB 1; Length 313;
Best Local Similarity 25.2%; Pred. No. 4.6;
Matches 39; Conservative 30; Mismatches 54; Indels 32; Gaps 9;

31 REKEFTVPDKLTE-----LGVISWRLNPDN-----ENCENLKRIREARGYSYVDICDVC 81
82 RVPMEVVLKKVSGSGVIRLLDWFEPDSFVLLERPEPVQ-----DLDFDI 133
83 PEKLPNYETIKISFFEEHLHTDEEIRYCLE-GSGYFDVRDNDQWIRALKKG-GMIVL 138
84 TERGAQEELARSEFFQVQL--EAVRHCHDGVLRHDKDEN---ILIDLNRGELKLIDF 187
139 PAGMYHRTLDTDNYIKAMRLFVGDVPVTPYNNRPH 173
188 GSGALLKDTVTVD--FDGTRVY-SPPEWIRYHYH 219

RESULT 12
SSGI_AVEA
ID SSGI_AVEA STANDARD; PRT; 518 AA.
AC P12615;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 01-FEB-1994 (Rel. 28, Last annotation update)
DE 12S seed storage globulin precursor.
OS Avena sativa (Oat).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae;
OC Avenaceae; Avena.
OX NCBI_TaxID=4498;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Williams;
RA Shotwell M.A., Afonso C., Davies E., Chesnut R.S., Larkins B.A.;
RT "Molecular characterization of oat seed globulins.";
RL Plant Physiol. 87:698-704 (1988).
CC -!- FUNCTION: THIS IS A SEED STORAGE PROTEIN.
CC -!- SUBUNIT: HEXAMER; EACH SUBUNIT IS COMPOSED OF AN ACIDIC AND A
```

SEQUENCE FROM N.A.
 RX MEDLINE=87277423; PubMed=3475233;
 RP Zakut-Houri R., Hazum S., Givol D., Telerman A.;
 RT "The cDNA sequence and gene analysis of the human pim oncogene.";
 RA Gene 54:105-111(1987).
 RL [3]
 RN
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=88217305; PubMed=3329709;
 RP Domen J., von Lindern M., Hermans A., Breuer M., Grosveld G.,
 RA Berns A.;
 RA "Comparison of the human and mouse PIM-1 cDNAs: nucleotide sequence
 RT and immunological identification of the in vitro synthesized PIM-
 RT and immunological identification of the in vitro synthesized PIM-
 RT and immunological identification of the in vitro synthesized PIM-
 RT and immunological identification of the in vitro synthesized PIM-

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protein.";
Oncogene Res. 1:103-112(1987).
[4]
SEQUENCE FROM N.A.
MEDLINE=88115604; PubMed=3429489;
Meeker T.C., Nagatajan L., Ar-Rushdi A., Croce C.M.;
"Cloning and characterization of the human PIM-1 gene: a putative
oncogene related to the protein kinases."
J. Cell. Biochem. 35:105-112(1987).
[5]
SEQUENCE OF 1-202 FROM N.A.
MEDLINE=21354098; PubMed=11460166;
Pasqualucci L., Nuneister P., Goossens T., Nanjangud G.,
Chaganti R.S.K., Kuppers R., Dalla-Favera R.;
"Hypomethylation of multiple proto-oncogenes in B-cell diffuse
large-cell lymphomas."
Nature 412:341-346(2001).
-1- CATALYTIC ACTIVITY: ATP + a protein = ADP + a phosphoprotein.
-1- TISSUE SPECIFICITY: EXPRESSED PRIMARILY IN CELLS OF THE
HEMATOPOIETIC AND GERM LINE LINEAGES.
-1- PTM: Autophosphorylated (By similarity).
-1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
PIM SUBFAMILY.
-1- DATABASE: NAME-Atlas Genet. Cytoenet. Oncol. Haematol.;
WWW="http://www.infobiogen.fr/services/chronocancer/Genes/PIMID261.html".
-----
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-----
EMBL; M27903; AAA60090.1; -
EMBL; M16750; AAA60089.1; -
EMBL; M54915; AAA36447.1; -
EMBL; M24779; AAA81553.1; -
EMBL; AF386792; AAK70871.1; -
PIR; A27476; TVHUPL
PIR; JU0327; JU0327.
PIR; A46554; A46554.
Gene; HGNC:8986; PIM1.
MIM; 164960; -
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_pkinase.
Pfam; PF00069; pkinase; 1.
ProDom; PD000001; Euk_pkinase; 1.
ProSITE; PS00107; PROTEIN_KINASE_ATP; 1.
ProSITE; PS00108; PROTEIN_KINASE_ST; 1.
ProSITE; PS50011; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; Proto-oncogene;
ATP-binding; Phosphorylation.
DOMAIN 38 290 PROTEIN KINASE.
NP_BIND 44 52 ATP (BY SIMILARITY).
BINDING 67 67 ATP (BY SIMILARITY).
ACT_SITE 167 167 BY SIMILARITY.
CONFLICT 15 16 AP -> RA (IN REF. 2).
SEQUENCE 313 AA; 35685 MW; 35BA76D3668E69A3 CRC64;
Query Match 7.4%; Score 81; DB 1; Length 313;
Best Local Similarity 25.2%; Pred. No. 6.8;
Matches 39; Conservative 29; Mismatches 55; Indels 32; Gaps 9;
Y 31 REPKEFIPVKLTE-----LGVISWRLNPDNW---ENCENLKRREARGSYVDICDVC 81
b 85 RVPMEVLLKKVSSGSGVIRLDWFERPDSFVLLERPEPVQ-----DLDFDI 133
Y 82 PEKLPNYETIKSFEEHLHTDEIRYCLE-GSGYFDVRDQNDQWIRIALKKG--GMIVL 138
b 134 TERGALQEELARSFFWQVL---EAVRHCHNCVGLHRDIKDN---ILIDLNRGELKLIDF 167
Y 139 PAGMYHRTDITDNYIKAMRLFVGDPVWTPYNRPH 173
b 188 GSGALLKDTVYTD--FDGTRVY-SPPEWIRYHRYH 219
Search completed: November 25, 2002, 10:09:17
Job time : 15 secs
```

45

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: November 25, 2002, 10:07:25 ; Search time 31 Seconds
(without alignments)
1322.690 Million cell updates/sec

Title: US-09-785-738a-2

Perfect score: 1097
Sequence: 1 MENEFOGKTEVIEAWYMD.....KEFLAKLLKSEGENQAVEGF 199

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

(SPTREMBL_21.4)

- 1: sp-archaea.*
- 2: sp-bacteria.*
- 3: sp-fungi.*
- 4: sp-human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp-mhc.*
- 8: sp-organalle.*
- 9: sp-phage.*
- 10: sp-plant.*
- 11: sp-rodent.*
- 12: sp-virus.*
- 13: sp-vertebrate.*
- 14: sp_unclassified.*
- 15: sp_virus.*
- 16: sp_bacteriap.*
- 17: sp-archeap.*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1097	100.0	199	10	O65035 oryza sativ
2	955.5	87.1	198	10	O81276 oryza sativ
3	946.5	86.3	198	10	Q93XJ5 hordeum vul
4	833.5	76.0	199	10	Q8W108 arabidopsis
5	789.5	72.0	940	10	O23327 arabidopsis
6	781	71.2	199	10	O48707 arabidopsis
7	680	62.0	185	10	Q9FG79 arabidopsis
8	609	55.5	179	11	Q99J79 mus musculu
9	586	53.4	179	4	Q9BV57 oryza sativ
10	581	53.0	179	4	Q9NV57 homo sapien
11	451	41.1	342	5	O9VTB1 drosophila
12	432	39.4	116	4	O9GP85 homo sapien
13	307.5	28.0	178	3	O94286 schizosacch
14	307.5	28.0	178	5	Q20340 caenorhabdi
15	287	26.2	71	10	Q93W70 musa acumin
16	229	20.9	221	5	Q09407 caenorhabdi

ALIGNMENTS

RESULT 1

O65035 PRELIMINARY; PRT; 199 AA.
AC O65035
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Submergence induced protein 2.
GN SIP2.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Ehrhartoideae; Oryzae; Oryza.
CX NCBI_TaxID=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA Lorbiecke R., Sauter M.;
RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF050200; AAC05511.1; -;
DR InterPro; IPR004313; Acired_dioxygenase.
DR Pfam; PF03079; ARD; 1.
SQ SEQUENCE 199 AA; 23601 MW; D1938253A1PC954D CRC64;

Query Match 100.0%; Score 1097; DB 10; Length 199;
Best Local Similarity 100.0%; Pred. No. 6.4e-94;
Matches 199; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MENEFOGKTEVIEAWYMDSEEDORLPHHREPKETIPVDKLTGLGVISWRLNPDNWC 60
|||||
DB 1 MENEFOGKTEVIEAWYMDSEEDORLPHHREPKETIPVDKLTGLGVISWRLNPDNWC 60
|||||
QY 61 ENLKRIREAGYSYVDICDVCPEKLPNYETIKISFFEEHLHTDEEIRYCLEGSGYFDVR 120
|||||
DB 61 ENLKRIREAGYSYVDICDVCPEKLPNYETIKISFFEEHLHTDEEIRYCLEGSGYFDVR 120
|||||
QY 121 QNDQWIRIALKKGNIIVLPAGMYHRTLDTDNYIKAMRLEFGVDPVWTPYNRPHDHPARK 180
|||||
DB 121 QNDQWIRIALKKGNIIVLPAGMYHRTLDTDNYIKAMRLEFGVDPVWTPYNRPHDHPARK 180
|||||

P91416 caenorhabdi
O31669 bacillus su
O61597 osteria
Q9b84 xylella fas
O67785 aquifex aeo
Q91341 pseudomonas
Q8vp0 synectococ
Q8ytj3 anabaena sp
Q9zfe7 klebsiella
Q9rm34 gluconobact
Q936j4 rhodospiril
Q18910 caenorhabdi
Q92t91 rhizobium m
Q99xq5 streptococ
O8t154 methanosarc
Q8tyw3 methanopyru
Q9skv9 arabidopsis
Q929t1 bacillus ha
O26046 helicobacte
Q08837 triticum ae
Q9f7g3 salmonella
Q9vq73 drosophila
P91740 hydra atten
Q8sv03 encephalito
Q9vx09 drosophila
Q9f0x5 mus musculu
Q97hf6 clostridium
Q9f7g4 salmonella
O66618 aquifex aeo


```

RESULT 5
O23327 ID O23327 PRELIMINARY; PRT; 940 AA.
AC O23327
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 108.0 kDa protein.
GN AT4G14710
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Stiekema W., Murphy G., Wambutt R., Pohl T., Terry N.,
RA Kreis M., Kavanagh T., Entian K.D., Rieger M., James R.,
RA Pulgomech P., Hatzopoulos P., Obermaier B., Duesterhoft A.,
RA Jones J., Palme K., Anson W., Delsen M., Bancroft I., Mewes H.W.,
RA Schueller C., Chalvatzis N.,
RA Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; 297336; CAB10250.1; -.
DR EMBL; AL161539; CAB78513.1; -.
DR InterPro; IPR004313; Acired_dioxygenase.
DR Pfam; PF03079; ARD; 2.
KW Hypothetical protein.
SQ SEQUENCE 940 AA; 107963 MW; 0451A8C9C4371179 CRC64;

Query Match 72.0%; Score 789.5; DB 10; Length 940;
Best Local Similarity 66.3%; Pred. No. 1.4e-64;
Matches 138; Conservative 26; Mismatches 15; Indels 29; Gaps 1;

QY 1 MENEFDQKTEVIAWYMDSEEDQRLPHHREPKEFIPVDKLTGLGVISWRNPNWENC 60
Db 1 MGEAVKQREVIQAWYMDSEEDQRLPHHREPKEFIPVDKLTGLGVISWRNPNWENC 60
QY 61 ENLKIRREARGSYV-----DIDCVCEKLPNYETK 91
Db 61 EDLKKIRSRGYSYVWCGLYFTIPLDLNGRCLFLSKSYFNSLGDCEVCCEKLPNYEVK 120
QY 92 IKSFFEEHLHTDEIRYCLESGYFVDRQNDQWIRIALKGGMIVLPAGMYHRTD 151
Db 121 VKSFFEEHLHTDEIRYCVAGTYGTVDRDRNEAIRVLVKKGGMIVLPAGTYHRTVDS 180
QY 152 NYIKAMRLFVGDVWTPYNNRPHDLPAR 179
Db 161 NYIKAMRLFVGPVWTPYNNRPHDLPAR 208

RESULT 6
O48707 ID O48707 PRELIMINARY; PRT; 199 AA.
AC O48707
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE At2g26400 protein.
GN AT2G26400.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RX MEDLINE=20083487; PubMed=10617197;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

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RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.-J., Roming C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome II of Arabidopsis thaliana.";
RL Nature 402:761-768(1999).
DR EMBL; AC002505; AAC14490.1; -.
DR InterPro; IPR004313; Acired_dioxygenase.
DR Pfam; PF03079; ARD; 1.
SQ SEQUENCE 199 AA; 23441 MW; 73053F8BC4ADEE25 CRC64;

Query Match 71.2%; Score 781; DB 10; Length 199;
Best Local Similarity 71.7%; Pred. No. 1.2e-64;
Matches 134; Conservative 27; Mismatches 26; Indels 0; Gaps 0;

QY 6 ODGKTEVIAWYMDSEEDQRLPHHREPKEFIPVDKLTGLGVISWRNPNWENC 65
Db 6 KDQTEEVIAWYMDSEEDQRLPHHREPKEFIPVDKLTGLGVISWRNPNWENC 65
QY 66 IREARGSYVDICDVCCEKLPNYETKIKSFEEHLHTDEIRYCLESGYFVDRQNDQW 125
Db 66 IRESRGYSYMDLCEVCCEKLPNYEKKVMEFEEHLHTDEIRYCLAGSYFVDRDLNDI 125
QY 126 IRIALKGGMIVLPAGMYHRTDTONYIKAMRLFVGDVWTPYNNRPHDLPARKEFLAK 185
Db 126 IRIWVKGGMIVLPAGMYHRTDTONYIKAMRLFVGDVWTPYNNRPHDLPARKEFLAK 185
QY 186 LKSEGE 192
Db 186 FLKVID 192

RESULT 7
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AC Q9FG79
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Genomic DNA, chromosome 5, pl clone:MOD19.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Katoh T., Asamizu E., Sato S., Nakamura Y., Kotani H.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. XI.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026651; BAB11314.1; -.
DR InterPro; IPR004313; Acired_dioxygenase.
DR Pfam; PF03079; ARD; 1.
SQ SEQUENCE 185 AA; 22263 MW; A4A4F594ED6BC2DA CRC64;

Query Match 62.0%; Score 680; DB 10; Length 185;
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Matches 116; Conservative 29; Mismatches 35; Indels 0; Gaps 0;

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Db 1 MQAWFMDSEEDQRLPHHREPKEFIPVDKLTGLGVISWRNPNWENC 60
QY 73 SYVDICDVCCEKLPNYETKIKSFEEHLHTDEIRYCLESGYFVDRQNDQWIRIALK 132
Db 61 DYMDLLDLCPEKVSNNYEKLNFEIHRDEIRYCLAGSYFVDRKDDIRIMQP 120
QY 133 GGMIVLPAGMYHRTDTONYIKAMRLFVGDVWTPYNNRPHDLPARKEFLAKLKEGE 192

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Db 121 GOLIVLPAGIYHRTLDASNYIKMLRLEVGPVWTPYNNRQSEHPVRKKYIHGLTYKFE 180

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ID Q99J79 PRELIMINARY; PRT; 179 AA.
AC Q99J79;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Similar to hypothetical protein FLJ10913.
GN AL024210.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005695; AAH05695.1; -.
DR MGI; MGI:2144929; AL024210.
DR InterPro; IPR004313; Acired_dioxgnase.
DR Pfam; PF03079; ARD; 1.
KW Hypothetical protein.
SQ SEQUENCE 179 AA; 21523 MW; 02CE7B89181EBEE CRC64;

Query Match 55.5%; Score 609; DB 11; Length 179;
Best Local Similarity 60.0%; Pred. No. 9.5e-49;
Matches 105; Conservative 32; Mismatches 38; Indels 0; Gaps 0;

QY 12 VIEAWYMDSEEDQRLPHHREPKFIPVDKLTGLGVISWRLNPDNWNENCKLRIRREARG 71
Db 1 MVQAWYMDSDAPCDPQHPDPGRPVGLQLRRLGVLYWKLADKYENDPELEKIRREARN 60

QY 72 YSYVDICDVCPEKLPNYETKIKSFEEHLHTDEIRYCLGSGYFDVRDQNDQWIRIALK 131
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QY 132 KGMVILPAGMYHRTLDTDNYIKAMRLFVGDVPVWTPYNNRPHDHLPAKKEFLAKLLK 189
Db 121 KGMVITLPAGIYHRTLDKKNYKAMRLFVGPVWTPYNNRPADHFEARGQTVKFLAOT 178

RESULT 9
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ID Q9BV57 PRELIMINARY; PRT; 179 AA.
AC Q9BV57;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical 21.5 kDa protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001467; AAH01467.1; -.
DR InterPro; IPR004313; Acired_dioxgnase.
DR Pfam; PF03079; ARD; 1.
KW Hypothetical protein.
SQ SEQUENCE 179 AA; 21498 MW; 92E13B9718D44C27 CRC64;

Query Match 53.4%; Score 586; DB 4; Length 179;
Best Local Similarity 56.7%; Pred. No. 1.3e-46;
Matches 101; Conservative 34; Mismatches 43; Indels 0; Gaps 0;

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RESULT 10
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AC Q9NV57;
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DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE OVARC100209 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RA Strausberg R.;
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC005695; AAH05695.1; -.
DR MGI; MGI:2144929; AL024210.
DR InterPro; IPR004313; Acired_dioxgnase.
DR Pfam; PF03079; ARD; 1.
KW Hypothetical protein.
SQ SEQUENCE 179 AA; 21483 MW; 3B67E975EAD68A1 CRC64;

Query Match 53.0%; Score 581; DB 4; Length 179;
Best Local Similarity 56.7%; Pred. No. 3.8e-46;
Matches 101; Conservative 33; Mismatches 44; Indels 0; Gaps 0;

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Db 1 MVLAWYMDSDAPCDPQHPDPGRPVGLQLRRLGVLYWKLADKYENDPELEKIRREARN 60

QY 72 YSYVDICDVCPEKLPNYETKIKSFEEHLHTDEIRYCLGSGYFDVRDQNDQWIRIALK 131
Db 61 YSWMDIITICKDLPNVEEKIKMEYEHLHLDDEIRYILDGSGYFDVRDQNDQWIRIFME 120

QY 132 KGMVILPAGMYHRTLDTDNYIKAMRLFVGDVPVWTPYNNRPHDHLPAKKEFLAKLLK 189
Db 121 KGMVITLPAGIYHRTLDKKNYKAMRLFVGPVWTPYNNRPADHFEARGQTVKFLAOT 178

RESULT 11
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ID Q9VTB1 PRELIMINARY; PRT; 342 AA.
AC Q9VTB1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE CG5000 protein.
GN CG7983 OR CG8000.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RA Strausberg R.;
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC001467; AAH01467.1; -.
DR InterPro; IPR004313; Acired_dioxgnase.
DR Pfam; PF03079; ARD; 1.
KW Hypothetical protein.
SQ SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
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[illegible]

JOURNAL Patent: WO 0161020-A 1 23-AUG-2001;
CropDesign N.V. (BE)

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BASE COUNT 267 a 176 c 206 g 223 t

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 8e-235;
Matches 872; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 AGACGACAAAAACAGAAATCCATGCCCATATATCGAAGGTTTCGCTTCCACCCCG 60
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DB 61 CAATCCACATGGAGAACGAAATCCAGAGTGGTAAGACGAGGTGATAGAACGATGTACA 120
QY 121 TGGATGATACGGAAGAGGACCGAGGCTTCCTCATCCCGCAACCCAAAGAAATCATTC 180
DB 121 TGGATGATACGGAAGAGGACCGAGGCTTCCTCATCCCGCAACCCAAAGAAATCATTC 180
QY 181 CTGTTGATAAGCTTACAGAACTAGGAGTAATCAGCTGGGCGCTTAATCTGTATACTGGG 240
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QY 721 TGCTATAGCAATGTAAATTTAGCACAGTGGCTATGTGCGCACTACCACTTTGAAGTGA 780
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QY 781 AAGATTTAATGATTTTGTAAATCTTATGATCAATCGCATATAGCATTTCCGAATG 840
DB 781 AAGATTTAATGATTTTGTAAATCTTATGATCAATCGCATATAGCATTTCCGAATG 840
QY 841 TGTTTTCAATAAACAGGAGTGCATGAAGCTGAA 872
DB 841 TGTTTTCAATAAACAGGAGTGCATGAAGCTGAA 872

RESULT 2
AF050200 872 bp mRNA linear PLN 12-MAR-1998
LOCUS Oryza sativa submergence induced protein 2 (sip2) mRNA, complete cds.
DEFINITION
ACCESSION AF050200 GI:2952337
VERSION AF050200
KEYWORDS
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
REFERENCE 1 (bases 1 to 872)
AUTHORS Lorbiecke, R. and Sauter, M.
TITLE Direct Submission
JOURNAL Submitted (24-FEB-1998) Department of General Botany, AMP II, University of Hamburg, Ohnhorststrasse 18, Hamburg 22609, Germany
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BASE COUNT 267 a 176 c 206 g 223 t

ORIGIN

Query Match 100.0%; Score 872; DB 8; Length 872;
Best Local Similarity 100.0%; Pred. No. 8e-235;
Matches 872; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGACGACAAAAACAGAAATCCATGCCCATATATCGAAGGTTTCGCTTCCACCCCG 60
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DB 61 CAATCCACATGGAGAACGAAATTCAGGATGGTAAGACGAGGTGATAGAACGATGTACA 120
QY 121 TGGATGATACGGAAGAGGACCGAGGCTTCCTCATCCCGCAACCCAAAGAAATCATTC 180
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QY 301 GTGATGTGTCGCCAGAGAGCTGCCAAATTTATGAACCTAAGATCAAGAGTTTCTTTGAAG 360
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QY 421 TGAGAGACCAAAATGATCAGTGGATTCGTATAGCACTGAAGAAAGGAGGATGATGTTTC 480
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QY 781 AAGATTTAATGATTTTCTTAATCTTATGATCAATCGGCATATAGCATTTCCCAATG 840
DB 781 AAGATTTAATGATTTTCTTAATCTTATGATCAATCGGCATATAGCATTTCCCAATG 840
QY 841 TGTTTCAATAACAGGAGTCATGAAGCTGAA 872
DB 841 TGTTTCAATAACAGGAGTCATGAAGCTGAA 872

RESULT 3
AX277506
LOCUS AX277506 980 bp DNA linear PAT 29-OCT-2001
DEFINITION Sequence 3 from Patent WO0161020.
ACCESSION AX277506
VERSION AX277506.1 GI:16549011
KEYWORDS
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1 Sauter, M.M. and Lorbiecke, R.
TITLE Alteration of growth and adaptation under hypoxic conditions
JOURNAL Patent: WO 0161020-A 3 23-AUG-2001;
CropDesign N.V. (BE)

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BASE COUNT 292 a 203 c 249 g 236 t

ORIGIN
Query Match 48.7% Score 424.4; DB 6; Length 980;
Best Local Similarity 83.3%; Pred. No. 1.4e-108;
Matches 495; Conservative 0; Mismatches 96; Indels 3; Gaps 1;

QY 67 ACATGGAGAACAATTCAGAGATGTAACAGCGAGGTGATAGAAGCATGTTACATCATGGATG 126
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QY 127 ATAGCTTACAGCACTAGGAGTAACTAGCTGGCGCTAAATCTCTGATATACTGGGCAATTT 186
DB 197 ACAGTGAAGAGGACAGAGGCTTCTCTCATCATCGTGAGGCCCAAGAAATTCATTCTCTT 256
QY 187 ATAGCTTACAGCACTAGGAGTAACTAGCTGGCGCTAAATCTCTGATATACTGGGCAATTT 246
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QY 247 GCGAGAACCTGAAGAGATCCGGAAGCCAGAGGTGTTACTCTTATGTTGGACATTTGTGATG 306
DB 317 ATGAGAACCTCAAGAAATCCGCGAGGCCAGGGGATACCTTACATGGGATATTTGTGATG 376
QY 307 TGTGCCAGAGAGAGCTGCCAAATTTATGAAATCAAGAGTTTCTTTGAAGAAACACC 366
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QY 367 TGCATACCGATGAAGAAATACGCTATTGCTTGAAGGAGTGGATACCTTTGATGTGAGAG 426
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RESULT 4
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LOCUS AF068332 980 bp mRNA linear PLN 10-JUN-1998
DEFINITION Oryza sativa submergence induced protein 2A mRNA, complete cds.
ACCESSION AF068332
VERSION AF068332.1 GI:3201968
KEYWORDS
SOURCE Oryza sativa.
ORGANISM Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

REFERENCE
1 (bases 1 to 980)
Lorbiecke, R. and Sauter, M.
TITLE Direct Submission
JOURNAL Submitted (26-MAY-1998) Department of General Botany, AMPII,
University of Hamburg, Ohnhorststrasse 18, Hamburg 22609, Germany

FEATURES
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BASE COUNT 292 a 203 c 249 g 236 t

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Best Local Similarity 83.3%; Pred. No. 1.4e-108;
Matches 495; Conservative 0; Mismatches 96; Indels 3; Gaps 1;
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Db 137 AGATGGAGAACGATTCACGAGGTGAAGACGGAGGTGATAGAGCATGTGTACATGGATG 196
QY 127 ATAGCGAAGAGGACGAGAGGCTTCCTCATCACCGCAACCCAAAGAAATTCATTCCTGTTG 186
Db 197 ACAGTGAAGAGGACGAGAGGCTTCCTCATCATCGTGAGCCCAAGAAATTCATTCCTCTTA 256
QY 187 ATAAGCTTACAGAACTAGGAGTAATCAGCTGGCGCCTAAATCTGTATACTGGGAGAATT 246
Db 257 GCAAACTTTCAGAGTTAGGAATATTAGCTGGCGCCTGAATGCTGTAGCTGGGAGAAATG 316
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Db 377 TGTGTCCAGAAAGCTGCCAAATATTGAGCTAAGCTAAGCTGAAATTTCTTTGAAGAACACT 436
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Db 437 TGCATACTATGAAGAGATACGCTATTGTCTTGAAGGAGTGGATCTTTCGATCGAGG 496
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QY 547 TTGTTGGCGATCTGTTTGGACACCTACACCGTCCCGCATGACCATCTTCTGCAAGAA 606
Db 617 TTGTTGGAGAGCTGTCTGGAGCGCGTACACCGTCCCGCATGACCATCTGCGAGCTAGAA 676
QY 607 AGGAGTTTTTGGCTAACTTCTCAAGTCAAGAGGTGAAATCAAGCAGTTGAAG 660
Db 677 AGGAGTATCGAAGAAATATCAA---CAGGGTGGAACTCAAGCTGTGGAAG 727

RESULT 5
AB025597
LOCUS AB025597 997 bp mRNA linear PLN 22-JUN-2001
DEFINITION Hordeum vulgare ID11 mRNA, complete cds.
ACCESSION AB025597
VERSION AB025597.1 GI:14522833
KEYWORDS
SOURCE Hordeum vulgare root cDNA to mRNA.

ORGANISM Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooidae; Triticeae; Hordeum.

REFERENCE 1 (sites)
Yanaguchi, H., Nakanishi, H., Nishizawa, N. K. and Mori, S.
Induction of the ID11 gene in Fe-deficient barley roots: a gene
encoding a putative enzyme that catalyses the methionine salvage
pathway for phytosiderophore production

JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

Soil Sci. Plant Nutr. 46, 1-9 (2000)
2 (bases 1 to 997)
Mori, S., Yanaguchi, H. and Nakanishi, H.
Direct Submission
Submitted (01-APR-1999) Satoshi Mori, Dept. Applied Biological
Chemistry, The University of Tokyo; 1-1 Yayoi, Bunkyo-ku, Tokyo
113-8657, Japan (E-mail: asmori@hongo.ecc.u-tokyo.ac.jp,
Tel: 81-3-5841-8137, Fax: 81-3-5841-8009)

FEATURES
source

1..997
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BASE COUNT 285 a 207 c 264 g 241 t

ORIGIN

Query Match 47.8%; Score 417.2; DB 8; Length 997;
Best Local Similarity 80.5%; Pred. No. 1.6e-106;
Matches 488; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
QY 35 GAAGGTTCGCTTGTCTTCCACCGCAATCCACATGAGAGCAATTCAGGATGGTAA 94
Db 46 GCATTTGCGCGGAGACTGCGAGGGCGCGCATGAGGAGAGTTCAGGATGGCAA 105
QY 95 GACGGAGGTGATAGAGCATGTTACATGATGATGAGAGAGGACGAGGCTTCTCTCA 154
Db 106 GGAGCAGGTATCCAAAGCATGTTACATGATGATGAGAGGACGAGGCTTCTCTCA 165
QY 155 TCACCGCGAACCAGAAATTCATTCCTGTTGATAGCTTACAGAACTAGAGTAATCAG 214
Db 166 TCACCGTGAAGCCAAAGAGTTCATTCCTTGCAGAACTTTCAGAACTAGGTTGTAAG 225
QY 215 CTGGCGCTTAAATCCCTGATAAATCGGAGAAATTCGAGAACTCAAGAGATCCGCGAAGC 274
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QY 275 CAGAGTTACTCTTATGTTGACATTTGTGATGTTGCTGCCAGAGAAAGTGCAGAAATATGA 334
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QY 395 TCTTGAGGAGTGGATACATTTGATGTGAGAGACCAAAATGATGATGATGATGATGATGATG 454
Db 406 TCTTGAGGAGTGGATACATTTGATGTGAGGAGCAAAACGAGGATGATGATGATGATGATGATG 465
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QY 635 ACAAGS 640

QY	573	TACAACCGTCCCATGACCATCTTCTGCAAGAACGAGTGTGTTTGGCTAAACTTCTCAAG	632
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QY	633	TCAGAAAGGTGAAAAATCAAGCAGTTGAAG	660
Db	597	GAGAAAGGTGTCGCCAAGCCGTTGATG	624
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AF462818			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
5'UTR			
CDS			

KEYWORDS
SOURCE
ORGANISM
 FLI_CDNA.
 thale cress.
 Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
AUTHORS
 Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,
 Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
TITLE
 Full-length messenger RNA sequences greatly improve genome
 annotation
JOURNAL
 Genome Biol. (2002) In press
REFERENCE
AUTHORS
 2 (bases 1 to 991)
 Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
 Feldmann,K.
TITLE
 Full-length cDNA from Arabidopsis thaliana
JOURNAL
 Unpublished
REFERENCE
AUTHORS
 3 (bases 1 to 991)
 Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
 Feldmann,K.
TITLE
 Direct Submission
JOURNAL
 Submitted (11-MAR-2002) Ceres, Inc, 3007 Malibu Canyon Road,
 Malibu, CA 90265, USA
COMMENT
 This clone sequence is one of 5,000 Ceres full-length cDNAs made
 available to TIGR and Genbank. The following quality assessment of
 this set was done by comparison with known proteins: two percent of
 the clones are estimated to be 5'-truncated; less than one percent
 are 3'-truncated; approximately two percent represent alternative
 splice variants, including unspliced introns and spliced exons; one
 percent may contain premature stop codons; five percent may have
 frame shifts in a coding region. A sequence is considered to be
 5'-truncated if it lacks the translation initiation start (ATG). A
 sequence is considered to be 3'-truncated if it lacks the
 C-terminal end of the encoded protein. Please note that these cDNA
 sequences are derived from the Ws or Laer ecotypes and therefore
 may contain polymorphisms when compared to sequences from Col-0.
 Genset carried out the library production and sequencing of the
 full-length clones. Ceres, Inc. carried out the clustering of the
 5' sequences, selection of clones, and sequence assembly.
FEATURES
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BASE COUNT 304 a 174 c 244 g 269 t
ORIGIN
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 Best Local Similarity 71.9%; Pred. No. 1.8e-76;
 Matches 406; Conservative 0; Mismatches 159; Indels 0; Gaps 0;
 QY 68 CATGGAGAACGAATCCAGGATGGTAAGACGGAGGTGATAGAACGATGGTACATGGATGA 127
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 QY 248 CGAAGACCTGAAGAGAAATCCCGGAAGCCAGAGGTTACTCTTATGTGGACATTTGTGATGT 307

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RESULT 10
AX449332 AX449332 1977 bp DNA linear PAT 03-JUL-2002
LOCUS Sequence 51 from Patent WO0185946.
DEFINITION AX449332
ACCESSION AX449332
VERSION AX449332.1 GI:21698079
KEYWORDS
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SOURCE
 ORGANISM Arabidopsis thaliana
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
REFERENCE
 1
AUTHORS
 Inze,D., Boudolf,V., de Veylder,L., Acosta,J.A. and Magyar,Z.
TITLE
 Nucleic acid molecules encoding plant cell cycle proteins and uses
 therefor
JOURNAL
 Patent: WO 0185946-A 51 15-NOV-2001;
FEATURES
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 Best Local Similarity 73.9%; Pred. No. 7.9e-75;
 Matches 387; Conservative 0; Mismatches 137; Indels 0; Gaps 0;
 QY 99 GAGGTGATAGAGCATGCTACATGATGATAGCGAAGAGGACGAGCTTCCTCATCAC 158
 DB 1162 GAAGTGATTCAGCTTGGTATATGATGATAGTAGTAAGAGGATCAGAGACTTCCTCACCAC 1221
 QY 159 CGCGAACCCAAAGAAATTCATTCTCTGTTGATTAAGCTTACAGAACTAGGAGTAATCAGCTGG 218
 DB 1222 AAGGATCCTAAAGAGTTTGTATCGTTGGACAACTTCAGAGCTGGGAGTACTTAGCTGG 1281
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BASE COUNT 270 a 164 c 205 g 250 t
ORIGIN

Query Match 32.8%; Score 285.6; DB 6; Length 889;
Best Local Similarity 68.3%; Pred. No. 2e-69;
Matches 396; Conservative 0; Mismatches 184; Indels 0; Gaps 0;
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Db 106 AAGACTCCGCCACACCAAGAAACCAAGGAGTTGTCTGTTGACCACACTTGTGAACT 165
Qy 203 AGGAGTAATCAGCTGGCGCCTTAATCTGTATGACTGGGAGAAATGCCAGAACCTGAAGAG 262
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Db 406 GATTTCGTGTGGTCAAGAAAGAGGAAATGATCATCTTACCTGCCGAATTTATCATCG 465
Qy 503 CTTTACGTTGGACACCGCAACTATATCAAGGCAATCGAGCTGTTTGTGGCGATCCTGT 562
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RESULT 13
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LOCUS
DEFINITION
Oryza sativa subsp. japonica BAC nbxb0006113, chromosome 10,
complete sequence.
AC027658
VERSION
AC027658.1 GI:7363409
KEYWORDS
HTG.
SOURCE
Oryza sativa.
ORGANISM
Oryza sativa
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
REFERENCE
1 (bases 1 to 142737)
AUTHORS
Liaca,V., Young,S., Kavchok,S., Clark,T., Choi,V.,
Nevill-Manning,C. and Messing,J.
Rice Chromosome 10
TITLE
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 142737)
AUTHORS
Liaca,V., Lou,A., Young,S., Charydczac,G., Choi,V.,
Nevill-Manning,C. and Messing,J.

TITLE Direct Submission
JOURNAL Submitted (31-MAR-2000) The Plant Genome Initiative at Rutgers -
Waksman Institute, Rutgers University, 190 Frelinghuysen Road,
Piscataway, NJ 08873
REFERENCE 3 (bases 1 to 142737)
AUTHORS
Liaca,V., Young,S., Kavchok,S., Clark,T., Charydczac,G., Choi,V.,
Nevill-Manning,C. and Messing,J.
TITLE Direct Submission
JOURNAL Submitted (02-APR-2000) The Plant Genome Initiative at Rutgers -
Waksman Institute, Rutgers University, 190 Frelinghuysen Road,
Piscataway, NJ 08873
REMARK Chromosome 10
FEATURES
Location/Qualifiers
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ORIGIN
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Best Local Similarity 96.7%; Pred. No. 6e-61;
Matches 261; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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LOCUS
DEFINITION
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AC086650
VERSION
AY086650.1 GI:21405360
KEYWORDS
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SOURCE
thale cress.
ORGANISM
Arabidopsis thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsi.
REFERENCE 1 (bases 1 to 759)
AUTHORS
Haas,B.J., Volfovsky,N., Town,C.D., Troukhan,M., Alexandrov,N.,
Feldmann,K.A., Flavell,R.B., White,O. and Salzberg,S.L.
Full-length messenger RNA sequences greatly improve genome
annotation
TITLE
JOURNAL
Genome Biol. (2002) In press
REFERENCE 2 (bases 1 to 759)
AUTHORS
Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
Full-length cDNA from Arabidopsis thaliana
JOURNAL
Unpublished
REFERENCE 3 (bases 1 to 759)
AUTHORS
Brover,V., Troukhan,M., Alexandrov,N., Lu,Y.-P., Flavell,R. and
Feldmann,K.
TITLE
Direct Submission

Qy	589	ACCATCTTCTGCAAGAAAGGAGTTTTTTGGCTAAACTTCTCAAGTCAGAGGTGAAAAATC	648
Db	499	AAGATCATCCAGCAGGAAAGGAGTACATCAAGAGTGTCTACTGAAAGAGTAGGAGTGCCTC	558
Qy	649	AAGCAG	654
Db	559	TTACAG	564

Search completed: December 1, 2002, 21:04:13
Job time : 3176 secs

PI Sauter MM, Lorbiecke R;
 XX WPI: 2001-529915/58.
 DR P-PSDB; AAE08929.
 XX
 PT New genetic constructs, comprising the SH2A or SH2A-like genes, useful
 for altering the growth and adaptation of plants under hypoxic
 PT conditions, e.g. improving water logging tolerance or regulating
 PT anaerobic response in plants -
 XX
 PS Example 2; Page 90-91; 107pp; English.
 XX
 CC The present invention relates to genetic constructs, which comprise a
 CC nucleotide sequence for an SH2A or SH2A-like gene, or an SH2A or SH2A-
 CC like protein gene promoter, where the SH2A or SH2A-like gene is operably
 CC linked to a promoter sequence that directs expression of the nucleotide
 CC sequence and the SH2A or SH2A-like protein gene promoter is operably
 CC linked to a heterologous coding sequence. The SH2A gene, initially
 CC identified in rice plants, is a submergence-induced early response gene
 CC which is involved in the adaptation of plants to hypoxic conditions
 CC (such as those encountered during submersion). In addition, the SH2A gene
 CC product has also been found to belong to a family of highly conserved
 CC proteins which occur ubiquitously in eukaryotes. The genetic constructs
 CC and methods are useful for altering the growth and adaptation of plants
 CC under hypoxic conditions. In particular, these are useful for improving
 CC water logging tolerance and regulating anaerobic response in plants.
 CC These are particularly useful in horticultural, agricultural, medical,
 CC fermentation and cell culture industries. The present sequence is rice
 CC SH2A cDNA.
 XX
 SQ Sequence 872 BP; 267 A; 176 C; 206 G; 223 T; 0 other;

Query Match 100.0%; Score 872; DB 22; Length 872;
 Best Local Similarity 100.0%; Pred. No. 7.2e-260;
 Matches 872; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AGAGCAACAAAACAGATCCATCCGATATCGAGAGGTTGCTTCTGCTCCACCCCG 60
 DB 1 AGAGCAACAAAACAGATCCATCCGATATCGAGAGGTTGCTTCTGCTCCACCCCG 60

QY 61 CAATCCACATGGAGAACGATTCAGGATGGTAAGACGAGGATAGAGCATGGTACA 120
 DB 61 CAATCCACATGGAGAACGATTCAGGATGGTAAGACGAGGATAGAGCATGGTACA 120

QY 121 TGGATGATACGAGAGGACGAGGTTCCATCATCCCGGACCCCAAGAAATTCATTC 180
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QY 181 CTGTTGATAGCTTACAGAACTAGGAGTAAATCAGCTGGCGCCTAAATCCTGATACCTGGG 240
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QY 361 AACACCTGCATACCGATGAAGAAATACGCTATTGCTTGAAGGAGTGGATACCTTTGATG 420
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 DB 481 TGCCTGCAGGGATGTACACCGCTTTACGTTGGACACCGCAACTATATCAAGGCAATGC 540

QY 541 GACTGTTTGTGGCGATCTCTGTTGGACACCCCTACAAACCGTCCCATGACCATCTTCCTG 600

DB 541 GACTGTTTGTGGCGATCTCTGTTGGACACCCCTACAAACCGTCCCATGACCATCTTCCTG 600
 QY 601 CAAGAAGAGAGTTTGGCTAAACTTCTCAAGTCAGAAGGTGAAAATCAAGCAGTTGAAG 660
 DB 601 CAAGAAGAGAGTTTGGCTAAACTTCTCAAGTCAGAAGGTGAAAATCAAGCAGTTGAAG 660
 QY 661 GCTTCTGAGGGTTTGTGGGCTCCTGCACTGCGGTCTCTATATTCACACCTGAATAAGATG 720
 DB 661 GCTTCTGAGGGTTTGTGGGCTCCTGCACTGCGGTCTCTATATTCACACCTGAATAAGATG 720

QY 721 TGTATAGCAATTAATTTAGCACAGTGGCTATGTCGCCACTCACCACCTGAAGTGA 780
 DB 721 TGTATAGCAATTAATTTAGCACAGTGGCTATGTCGCCACTCACCACCTGAAGTGA 780

QY 781 AAGATTTAATGATTTTGTAAATCTTATGTCATCAATCGGCATATAGCATTTCCGAAATG 840
 DB 781 AAGATTTAATGATTTTGTAAATCTTATGTCATCAATCGGCATATAGCATTTCCGAAATG 840

QY 841 TGTTCATTAACACAGAGTTCATGAAGCTGAA 872
 DB 841 TGTTCATTAACACAGAGTTCATGAAGCTGAA 872

RESULT 2
 AAD15648
 ID AAD15648 standard; cDNA; 980 BP.
 XX
 AC AAD15648;
 XX
 DT 15-NOV-2001 (first entry)
 XX
 DE Rice submergence-induced early response gene SH2B (EST S2993).
 XX
 KW Rice; SH2A; submergence induced early response gene; anaerobic response;
 KW water logging tolerance; hypoxic environment; horticultural;
 KW agricultural; medical; fermentation; cell culture industry;
 KW genetic construct; transgenic plant; EST S2993; expressed sequence tag;
 KW ss.
 XX
 OS Oryza sativa.
 XX
 FH Key Location/Qualifiers
 FT CDS 139..735
 FT /*tag= a
 FT /product= "Rice SH2B protein"
 XX
 PN WO200161020-A2.
 XX
 PD 23-AUG-2001.
 XX
 PF 16-FEB-2001; 2001WO-IB00745.
 XX
 PR 18-FEB-2000; 2000US-0183572.
 XX
 PA (CROP-) CROPDESIGN NV.
 XX
 PI Sauter MM, Lorbiecke R;
 XX
 DR WPI: 2001-529915/58.
 DR P-PSDB; AAE08930.
 XX
 PT New genetic constructs, comprising the SH2A or SH2A-like genes, useful
 for altering the growth and adaptation of plants under hypoxic
 PT conditions, e.g. improving water logging tolerance or regulating
 PT anaerobic response in plants -
 XX
 PS Example 3; Page 92-93; 107pp; English.
 XX
 CC The present invention relates to genetic constructs, which comprise a
 CC nucleotide sequence for an SH2A or SH2A-like gene, or an SH2A or SH2A-
 CC like protein gene promoter, where the SH2A or SH2A-like gene is operably
 CC linked to a promoter sequence that directs expression of the nucleotide

CC sequence and the SH2A or SH2A-like protein gene promoter is operably
CC linked to a heterologous coding sequence. The SH2A gene, initially
CC identified in rice plants, is a submergence-induced early response gene
CC which is involved in the adaptation of plants to hypoxic conditions
CC (such as those encountered during submersion). In addition, the SH2A gene
CC product has also been found to belong to a family of highly conserved
CC proteins which occur ubiquitously in eukaryotes. The genetic constructs
CC and methods are useful for altering the growth and adaptation of plants
CC under hypoxic conditions. In particular, these are useful for improving
CC water logging tolerance and regulating anaerobic response in plants.
CC These are particularly useful in horticultural, agricultural, medical,
CC fermentation and cell culture industries. The present sequence is a rice
CC SH2A-like cDNA, SH2B, obtained from EST (expressed sequence tag) S2993.
XX
SQ Sequence 980 BP; 292 A; 203 C; 249 G; 236 T; 0 other;

Query Match 48.7%; Score 424.4; DB 22; Length 980;
Best Local Similarity 83.3%; Pred. No. 5.3e-121;
Matches 495; Conservative 0; Mismatches 96; Indels 3; Gaps 1;

Qy 67 ACATGGAGAGCAATTCAGGATGTTAAGCAGGAGGTGATAGAACGATGGTACATGGATG 126
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 137 AGATGGAGCAACAGTTCAGGATGCGAAGGAGGAGTTCATCGAAGCTTGGTACATGGATG 196
Qy 127 ATAGCGAAGAGACAGAGGCTTCCTCATACCGCGAACCCAAAGAAATTCATTCCTGTG 186
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 197 ACAGTGAAGAGACAGAGGCTTCCTCATCATCGTGAGGCCAAAGAAATTCATTCCTCTTA 256
Qy 187 ATAGCTTACAGAACTAGAGTAATCAGTCTGCGGCTTAATCTCTAATACCTGGGAGAAAT 246
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 257 GCAAACTTTCAGAGTTAGGAATATTAAGCTGCGGCTGAATGCTGATGACTGGGAGATG 316
Qy 247 CGGAGAACTGAAGAGATCCCGAAGCCAGAGGTTACTTCTATGCGACATTTGTGATG 306
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 317 ATGAGAACTCAAGAAATCCGTGAGGCCAGGGGATACCTTTACATGGATATTTGTGATG 376
Qy 307 TGTGCCAGAGAGCTGCCAAATTAAGAACTAAGAGTTTCTTTGAAGAACAC 366
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 377 TGTGTCAGAAAGCTGCCAACTATGAGGCTAAGCTGNAATTTCTTTGAAGAACACT 436
Qy 367 TGCATPACCGATGAAGAATACGCTATTGCTTTGAAGGAGTGGATACTTTGTGATGAGAG 426
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 437 TGCATPACTGATGAAGATACGCTATTGCTTTGAGGGAAGTGATGATCTCGATGTCAGGG 496
Qy 427 ACCAAATGATCAGTGGATTCGTATAGCACTCAAGAAAGAGGAGCATGTTGTCGCTG 486
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 497 ACCAAATGATCAGTGGATTCGTATAGCACTCAAGAAAGGAGGAGCATGTTGTCGCTG 556
Qy 487 CAGGATGTACCAACCGCTTACGTTGGACACCGACAACTATATCAAGGCAATGCGACTGT 546
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 557 CGGGAATGTATCACCGCTTACATTTGGACAGTGACAACTACATCAAGGCAATGCGGCTCT 616
Qy 547 TTGTTGGCGATCCTTTTGGACACCTCAACCGTCCCATGACCATCTTCCTGCAAGAA 606
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 617 TTGTGGGAGAGCTGTCTGGACCGCTCAACCGTCCCATGACCATCTGCGAGCTAGAA 676
Qy 607 AGGAGCTTTTGGCTAAACTTCTCAAGTCAGAGGTGCAAAATCAAGCAGTTGAAG 660
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 677 AGGAGTATGCTCGAAAAAATATCAA---CAGGGGTGAACTCAAGCTGTGCGAAG 727

RESULT 3
AADI5652
ID AADI5652 standard; DNA; 933 BP.
XX
AC AADI5652;
XX
DT 15-NOV-2001 (first entry)
XX Cotton submergence-induced early response gene SH2A-like DNA.
XX
KW Cotton; SH2A-like protein; submergence induced early response gene;
KW anaerobic response; water logging tolerance; hypoxic environment;

KW horticultural; agricultural; medical; fermentation;
KW cell culture industry; genetic construct; transgenic plant; ds.
XX
OS Gossypium hirsutum.
FH Key Location/Qualifiers
CDS 33..535
FT /*tag= a
FT /product= "cotton SH2A-like protein"
XX
PN WO200161020-A2.
PD 23-AUG-2001.
XX
PF 16-FEB-2001; 2001WO-IB00745.
XX
PR 18-FEB-2000; 2000US-0183572.
XX
PA (CROP-) CROPDESIGN NV.
XX
PI Sauter MM, Lorbiecke R;
XX
DR WPI: 2001-529915/58.
DR P-PSDB; AAE08934.
XX
PT New genetic constructs, comprising the SH2A or SH2A-like genes, useful
PT for altering the growth and adaptation of plants under hypoxic
PT conditions, e.g. improving water logging tolerance or regulating
PT anaerobic response in plants -
XX
PS Claim 31; Page 100-101; 107pp; English.
XX
CC The present invention relates to genetic constructs, which comprise a
CC nucleotide sequence for an SH2A or SH2A-like gene, or an SH2A or SH2A-
CC like protein gene promoter, where the SH2A or SH2A-like gene is operably
CC linked to a promoter sequence that directs expression of the nucleotide
CC sequence and the SH2A or SH2A-like protein gene promoter is operably
CC linked to a heterologous coding sequence. The SH2A gene, initially
CC identified in rice plants, is a submergence-induced early response gene
CC which is involved in the adaptation of plants to hypoxic conditions
CC (such as those encountered during submersion). In addition, the SH2A gene
CC product has also been found to belong to a family of highly conserved
CC proteins which occur ubiquitously in eukaryotes. The genetic constructs
CC and methods are useful for altering the growth and adaptation of plants
CC under hypoxic conditions. In particular, these are useful for improving
CC water logging tolerance and regulating anaerobic response in plants.
CC These are particularly useful in horticultural, agricultural, medical,
CC fermentation and cell culture industries. The present sequence is a
CC cotton SH2A-like DNA.
XX
SQ Sequence 933 BP; 268 A; 157 C; 223 G; 285 T; 0 other;

Query Match 38.9%; Score 339.2; DB 22; Length 933;
Best Local Similarity 74.8%; Pred. No. 1.4e-94;
Matches 425; Conservative 0; Mismatches 143; Indels 0; Gaps 0;

Qy 93 AGACCGAGGTGATAGACATGGTACATGGATGATAGCAAGAGGACGAGCTTCCT 152
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 57 AGGCGGAAGTTATTCAGGATGCTACATGATGATGATGATGATGATGATGATGATGATG 116
Qy 153 CATCACCGCGAACCCCAAGAAATTCATTCCTGTTGATAGCTTACAGAACTAGGAGTAATC 212
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 117 CATCACCGTGAACCTTAAGGAATATGATCTCTGATAACTTGTGAGCTTGGAGTACTC 176
Qy 213 AGCTGGCGCTAAATCCTGATAACTGGGAGAATTCGAGAACCTTGAAGAGATCCCGGAA 272
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 177 AGCTGGCGATGGATGCTGATAACTATGAAATGATGAAGATGGAAGAAATTCGTGAA 236
Qy 273 GCCAGAGGTTACTCTTATGTGGACATTTGTGATGTGCCCGAGAGAGCTGCCAAATAT 332
Dy | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Dy 237 GAACGAGGTTACTCCTACATGGAGCTTCTGCGAGGTTTGCCTTGAGAGCTTCCAAATAT 296
Qy 333 GAAACTAAGATCAAGAGTTCTTTTGAAGAACACCTGCTGATCCCGATGAAGAAATACGTTAT 392

PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151085.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159283.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.

PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161992.
PR 29-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 36.0%; Score 313.8; DB 21; Length 989;
Best Local Similarity 72.2%; Pred. No. 1.le-86;
Matches 408; Conservative 0; Mismatches 157; Indels 0; Gaps 0;

QY 68 CATGGAGAAGAAATCCAGGATGTAAGACGGAGGTGATAGAGCATGTACATGGATGA 127
 ||||| ||||| ||||| ||||| |||||
Db 193 CATGGGTGAAGTGGTGAAGAGGAAGAAAGTATCCAGGCATGGTATATGATGA 252

QY 128 TAGCGAAGAGGACAGAGGCTTCCTCATCCCGCGCAACCCAAAGAAATTCATCTCTGGA 187
 ||||| ||||| ||||| ||||| |||||
Db 253 TAGCGAAGAGGATCAGAGACTTCCTCACCACAAGGATCTTAAGGAGCTTCTATCTTTGGA 312

QY 188 TAAGCTTACAGAACTAGGAGTAATCAGCTGGCGCTTAATCTCTATGCTGGACATTTGTGATGT 247
 ||| ||| ||| ||| ||| |||
Db 313 CAACTTGCAGAGCTGGGAGTACTTAGCTGGAGACTTGATGCTGATAACTATGAAACCGA 372

QY 248 CGAGAACCTGAAGAGAAATCCGCGAAGCCAGAGGTTACTCTTATGCTGGACATTTGTGATGT 307
 ||| ||| ||| ||| ||| |||
Db 373 TGAGGATTTGAAAAGATCCGCAATCTCGTGTACTCTTACATGGACTTTTGTGAGGT 432

QY 308 GTGCCAGAGAAGCTGCCAAATTTATGAAACTAAGATCAAGAGTTTCTTTGAACAACACCT 367
 ||||| ||||| ||||| ||||| |||||
Db 433 ATGCCCGGAAAAGCTTCCAACATATGAAGTGAAGTGAAGAGCTTTTTCGAAGAACATTT 492

QY 368 GCATACCGATGAAGAAATACGCTATTGTCTTGAAGGGAGTGGATACTTTGATGTGAGAGA 427
 ||| ||| ||| ||| ||| |||
Db 493 GCACACTGATGAAGAGATCCGTTACTGCTGCGTGCAGGAGCGGTTACTTTGATGTGAGGA 552

QY 428 CCAAAATGATGAGTGGATTCGTATAGCACTGAAGAAAGGAGGATGATGTTCTGCTGTC 487
 ||| ||| ||| ||| ||| |||
Db 553 TCGCAATGAAGCTTGGATTAGATATGGGTAAAGAAAGGGAGGTATGATAGTCTTACCTGC 612

QY 488 AGGATGTACACCGCTTTACGTTGGACACCGACACTATATCAAGGCATGCGACTGTT 547
 ||| ||| ||| ||| ||| |||
Db 613 TGAATATATATCATCGCTTCCACCGTAGACTCAGACAACATATATCAAGGCAATGCGGCTTT 672

QY 548 TGTGGCGATCTGTTTGGACACCTTACAAACCGTCCCATGACCATCTTCTCTGCAAGAAA 607
 ||||| ||| ||| ||| ||| |||
Db 673 CGTTGTGAACCGGCTGAGACACCATACAAATCGCCACACGACCACTCCCTGCAAGGAA 732

QY 608 GGAGTTTTTGGCTAAACTTCTCAAG 632
 ||| ||| ||| ||| ||| |||
Db 733 AGAGTACATCGATAATTTCTGTGAAG 757

RESULT 5
AAC48247
ID AAC48247 standard; DNA; 1539 BP.
XX AAC48247;
AC AAC48247;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 56793.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX Arabidopsis thaliana.
OS
XX
PN EP1033405-A2.
PD 06-SEP-2000.
XX

PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 03-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
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PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134370.
PR 18-MAY-1999; 99US-0134376.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
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PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
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PR 18-JUN-1999; 99US-0139750.
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PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
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PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
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PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
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XX AC AAC43654;
XX DT 18-OCT-2000 (first entry)
XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 40010.
XX KW Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway;
XX KW metabolic pathway; promoter; termination sequence; ss.
XX OS Arabidopsis thaliana.
XX PN EP1033405-A2.
XX PD 06-SEP-2000.
XX PF 25-FEB-2000; 2000EP-0301439.
XX PR 25-FEB-1999; 99US-0121825.
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Db	255	TAGCGAAGAGGATGAGACTTCCTCCACCAAGGATCCTTAAGAGGATTCCTATCTTTTGA	314
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DT	01-AUG-2002 (first entry)		
XX	Arabidopsis thaliana expressed polynucleotide SEQ ID NO 629.		
DE	Arabidopsis thaliana; plant; insecticide; fungicide; transgenic; stress;		
KW	disease; crop; thale cress; tolerance factor; insect; pathogen;		
KW	nutrition; ds.		
XX	Arabidopsis thaliana.		
OS	US2002023281-A1.		
PN	21-FEB-2002.		
XX	26-JAN-2001; 2001US-0770445.		
PF	27-JAN-2000; 2000US-178472P.		
XX	(GORL/) GORLACH J.		
PA	(ANY/) AN Y.		
PA	(HAM/) HAMILTON C M.		
PA	(PRIC/) PRICE J L.		
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PA	(MATH/) MATHAW A V.		
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(HOFF/) HOFFMAN N.
(HURB/) HURBAN P.
Gorlach J, An Y, Hamilton CM, Price JL, Raines TM, Yu Y;
Rameaka JG, Page A, Mathew AV, Ledford BL, Woessner JP, Haas WD;
Garcia CA, Krickler M, Slater T, Davis KR, Allen K, Hoffman N;
Hurban P;
WPI: 2002-400781/43.
New Arabidopsis thaliana nucleic acid for identifying homologous genes,
producing compositions that modulate the expression or function of its
encoded protein, and mapping functional regions of protein -
Claim 1: SEQ ID NO 629; 49pp + Sequence Listing; English.
The invention relates to an Arabidopsis thaliana nucleic acid (I)
comprising a sequence capable of hybridising under stringent conditions
to a sequence selected from any one of 999 sequences (ABN98233-ABN99231),
given in the specification or its fragment. A polypeptide (II) encoded by
(I), a transgenic plant (III) comprising an exogenous nucleic acid or a
genetically modified cell (IV) comprising an exogenous nucleic acid, is
useful for screening a candidate agent for its biological effect. (I) is
useful in identifying homologous or related genes, in producing
compositions that modulate the expression or function of its encoded
protein, mapping functional regions of the protein and in studying
associated physiological pathways. (I) is also useful for the genetic
manipulation of cells, particularly plant cells. (I) is also useful in
screening assays of various plant strains to determine the strains that
are best capable of withstanding a particular disease or environmental
stress. (II) and (III) are useful for screening of biologically active
agents, e.g. fungicides, insecticides, etc., for elucidating biochemical
pathways. The screened agents are useful in improved methods of treating
crops to prevent or treat disease. (II) are also useful in screening
programs to identify agents that mimic or enhance the action of tolerance
factors. Such agents are useful in improved methods of treating crops to
enhance their tolerance to environmental stress. (I) is also useful
for enhancing or inhibiting production of a biosynthetic product in a
plant. (III) is useful for identifying other mediators that may induce
expression of proteins of interest, for establishing the extent to which
any specific insect and/or pathogen is responsible for damage to a
particular plant, for identifying other mediators that enhance or induce
tolerance to environmental stress, for identifying factors involved in
biosynthetic pathways of nutritional, commercial, or medicinal value and
for identifying productions of nutritional, commercial or medicinal
value. (IV) is useful in the study of genetic function and regulation,
for alteration of the cellular metabolism and for screening compounds
that may affect the biological function of the gene or gene products.
Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from USPTO
at seqdata.uspto.gov/sequence.html?DocID=999909770445.
Sequence 849 BP; 252 A; 190 C; 151 G; 247 T; 9 other;
Query Match 35.2%; Score 307; DB 24; Length 849;
Best Local Similarity 72.4%; Pred. No. 1.3e-84;
Matches 391; Conservative 0; Mismatches 149; Indels 0; Gaps 0;
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ID AAS96322 standard; cDNA; 1977 BP.
XX AAS96322;
AC AAS96322;
XX 26-FEB-2002 (first entry)
DT Arabidopsis cDNA encoding cell cycle protein CCP22.
DE Arabidopsis thaliana.
XX Cell cycle protein; CCP; ss; cell cycle regulation; herbicide;
KW plant growth regulator; plant development; abiotic stress; biotic stress;
KW nutrient deprivation; pathogen attack; crop yield.
XX Arabidopsis thaliana.
OS Arabidopsis thaliana.
XX WO200185946-A2.
PN 15-NOV-2001.
XX 14-MAY-2001; 2001WO-IB01307.
XX 12-MAY-2000; 2000US-204045P.
PR (CROP-) CROPDESIGN NV.
PA Inze D, Boudolf V, De Veylder L, Acosta JAT, Magyar Z;
PI WPI; 2002-062249/08.
XX P-PSDB; AAU72532.
DR New cell cycle protein and nucleic acid molecule encoding it useful for
XX regulating cell cycle progression in plants and for identifying
PT modulators which are useful as herbicides or plant growth regulators -
XX Claim 38; Fig 22; 316pp; English.
XX The invention relates to a novel cell cycle protein (CCP) and the
CC polynucleotides encoding them. CCP is useful for identifying a compound
CC which modulates the activity of the polypeptide and which binds to the
CC polypeptide and an anti-CCP antibody is useful for detecting the presence
CC of CCP in a sample. A CCP modulator is useful for modulating the cell
CC cycle or growth of a plant such as Arabidopsis thaliana, rice, wheat,
CC maize, tomato, alfalfa, oilseed rape, soybean, sunflower and canola.
CC CCP nucleic acid and polypeptide molecules are useful as modulating
CC agents in regulating cell cycle progression in plants. CCP is useful to
CC treat disorders characterised by insufficient or excessive production of
CC CCP protein or production of CCP protein forms which have decreased or
CC aberrant activity. Compounds that bind to or modulate the activity
CC of CCP polypeptide are useful as herbicides or plant growth regulators.
CC The polynucleotide is useful for modifying cell fate, plant development,


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PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
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PR 31-AUG-1999; 99US-0151438.
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Query Match 34.8%; Score 303.2; DB 21; Length 925;

Best Local Similarity 72.9%; Pred. No. 2e-83;

Matches 404; Conservative 0; Mismatches 148; Indels 2; Gaps 1;

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Qy 129 AGCGAAGAGGACCGAGGCTCTCATCACCCGACCCAAAGAAATTCATTCTCTTGTAT 188
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QY 549 GTTGGCGATCCTGTTTGGACACCCCTACAAACCGTCCCCCATGACCATCTTCTGCAAGAAAG 608
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Db 617 GAATATGTCGATAA 630

RESULT 12
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AC AAC43125;
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DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana DNA fragment SEQ ID NO: 38120.
XX
KW Hybridisation assay; genetic mapping; gene expression control;
KW protein identification; signal transduction pathway;
KW metabolic pathway; promoter; termination sequence; ss.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Query Match 34.6%; Score 301.6; DB 21; Length 600;
Best Local Similarity 70.9%; Pred. No. 5e-83;
Matches 400; Conservative 0; Mismatches 164; Indels 0; Gaps 0;

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Db 1 ATGGGTGAAGCCGCTAAGGATCAAACTGAAGAAGTGATTCAAGCTTGCTACTTGGATAAT 60

QY 129 AGCGAAGAGGACAGAGGCTTCCTCATCCCGGCAAGCCAAAGAACCAAGAAATTCATTCCTTTGAT 188
| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 AAGGAAGAGGATCAGAAACTTCCTCACCACAAGGATCCTAAGGAATTTGTATCTTTGGAC 120

QY 189 AAGCTTACAGAACTAGGAGTAATCAGCTGGCGCCTAAATCCTGATACTGGAGAAATTCG 248
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Db 121 AAACCTTGCAAGCTTGGAGTACTTTTGTGGAGACTTGATGCTGATAACTATGAAACCGAT 180

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RESULT 13

AAC41735

ID AAC41735 standard; DNA; 597 BP.

XX AC AAC41735;

XX AC AAC41735;

XX DT 17-OCT-2000 (first entry)

XX DE Arabidopsis thaliana DNA fragment SEQ ID NO: 32942.

XX KW Hybridisation assay; genetic mapping; gene expression control;
XX KW protein identification; signal transduction pathway;
XX KW metabolic pathway; promoter; termination sequence; ss.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

XX PR 05-MAR-1999; 99US-0123180.

XX PR 09-MAR-1999; 99US-0123548.

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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.

PR	07-OCT-1999;	99US-0158029.	
PR	08-OCT-1999;	99US-0158232.	
PR	12-OCT-1999;	99US-0158369.	
PR	13-OCT-1999;	99US-0159293.	
PR	13-OCT-1999;	99US-0159294.	
PR	13-OCT-1999;	99US-0159295.	
PR	14-OCT-1999;	99US-0159329.	
PR	14-OCT-1999;	99US-0159330.	
PR	14-OCT-1999;	99US-0159331.	
PR	14-OCT-1999;	99US-0159637.	
PR	14-OCT-1999;	99US-0159638.	
PR	18-OCT-1999;	99US-0159584.	
PR	21-OCT-1999;	99US-0160741.	
PR	21-OCT-1999;	99US-0160767.	
PR	21-OCT-1999;	99US-0160768.	
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PR	21-OCT-1999;	99US-0160814.	
PR	21-OCT-1999;	99US-0160815.	
PR	22-OCT-1999;	99US-0160980.	
PR	22-OCT-1999;	99US-0160981.	
PR	22-OCT-1999;	99US-0160989.	
PR	25-OCT-1999;	99US-0161404.	
PR	25-OCT-1999;	99US-0161405.	
PR	25-OCT-1999;	99US-0161406.	
PR	26-OCT-1999;	99US-0161359.	
PR	26-OCT-1999;	99US-0161360.	
PR	26-OCT-1999;	99US-0161361.	
PR	28-OCT-1999;	99US-0161920.	
PR	28-OCT-1999;	99US-0161992.	
PR	28-OCT-1999;	99US-0161993.	
PR	29-OCT-1999;	99US-0162142.	

Query Match

Best Local Similarity

Matches 405; Conservative

33.1%;

70.8%;

0; Mismatches 149; Indels 18; Gaps 1;

Score 288.2; DB 21; Length 597;

Pred. No. 7.2e-79;

Qy	69	ATGGAGAACGAATTCACGAGTGGTAAGACGGAGGTGATAGAAAGCATGTACATGGATGAT 128
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Db	61	AGTGAAGAGGATCAGACAGCTTCCTCACCACAAGGATCCTAAAGAGTTGTATCGTTGGGC 120
Qy	189	AAGCTTACAGAACTAGGAGTAATCAGCTGGCGCCTAAATCCTGTATACTGGGAGAAATGCC 248
Db	121	AAACTTGCAGAGCTGGGAGTACTTACGCTGGAGACTTGATGCTGATACTACGAAACCGAT 180
Qy	249	GAGAACCTGAAGAGAAATCCGCGAAGCCAGAGGTTACTCTTA-----T 290
Db	181	GAGGATTTGAAAAGATCCGTGAATCTCGTGGTTACTCTTACATGAAAATGTTCAAATT 240
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Db	241	CAGGACTTTTGTGAGGTATGCCGCGAAAAGCTTCCAAACTATGAAGTGAAGCTAAAGAGC 300
Qy	351	TTCTTTGAAGAACACCTGCATACCGATGAAGAAATACGCTATTGCTTTGAAGGGAGTGA 410
Db	301	TTTTTCGAAGAACATTTGCATACTGATGAAGAGATCCGTTACTGCGTTGCAGGAAGTGT 360
Qy	411	TACTTTGATGTGAGAGACCAAAATGATCAGTGGATTCGTTATAGCACTGAAGAAAGAGGC 470
Db	361	TACTTTGATGTGAGAGATGCGCAATGAAGCTTAGGTTAGGTTAGGTTAAAGAGGAGCT 420
Qy	471	ATGATTTGTTCTCCCTGCAAGGATGTACCACCGCTTTACGTTGGACACCGACCACTATATC 530
Db	421	ATGATAGTCTTACCTGCTGGGATCTATCATCGCTTACCGTGGACTCTGACAACTATATC 480
Qy	531	AAGGCAATGCGACTGTTGTTGGCGATCCTGTTGGACACCCCTACAACCGTCCCCATGAC 590
Db	481	AAGGCAATGCGGCTTTTCGTGGGTGAACCGGTATGGACACCATACAAATCGCCACACGAC 540
Qy	591	CATCTTCTCGAAGAAAGAGTTTTTTGGCTAA 622

Db	541	CATCTTCTCGAAGAAAGATATGTCGATAA 572	
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ID	AAAD15651	standard; DNA; 889 BP.	
XX	AAAD15651;		
DT	15-NOV-2001	(first entry)	
DE	Soybean submergence-induced early response gene SH2A-like DNA.		
KW	Soybean; SH2A-like protein; submergence induced early response gene;		
KW	anaerobic response; water logging tolerance; hypoxic environment;		
KW	horticultural; agricultural; medical; fermentation;		
KW	cell culture industry; genetic construct; transgenic plant; ds.		
OS	Glycine max.		
XX			
XX	Key	Location/Qualifiers	
FT	CDS	2..634	
FT		/*tag= a	
FT		/product= "Soybean SH2A-like protein"	
FT		/note= "CDS does not include start codon"	
FT		/partial	
XX	WO200161020-A2.		
XX	23-AUG-2001.		
XX	16-FEB-2001;	2001WO-1B00745.	
XX	18-FEB-2000;	2000US-0183572.	
XX	(CROP-) CROPDESIGN NV.		
XX	Sauter MM,	Lorbiecke R;	
XX	WPI; 2001-529915/58.		
XX	P-PSDB; AAE08933.		
XX	New genetic constructs, comprising the SH2A or SH2A-like genes, useful		
XX	for altering the growth and adaptation of plants under hypoxic		
XX	conditions, e.g. improving water logging tolerance or regulating		
XX	anaerobic response in plants		
XX	Claim 31;	Page 98-99; 107pp; English.	
XX	The present invention relates to genetic constructs, which comprise a		
XX	nucleotide sequence for an SH2A or SH2A-like gene, or an SH2A or SH2A-		
XX	like protein gene promoter, where the SH2A or SH2A-like gene is operably		
XX	linked to a promoter sequence that directs expression of the nucleotide		
XX	sequence and the SH2A or SH2A-like protein gene promoter is operably		
XX	linked to a heterologous coding sequence. The SH2A gene, initially		
XX	identified in rice plants, is a submergence-induced early response gene		
XX	which is involved in the adaptation of plants to hypoxic conditions		
XX	(such as those encountered during submersion). In addition, the SH2A gene		
XX	product has also been found to belong to a family of highly conserved		
XX	proteins which occur ubiquitously in eukaryotes. The genetic constructs		
XX	and methods are useful for altering the growth and adaptation of plants		
XX	under hypoxic conditions. In particular, these are useful for improving		
XX	water logging tolerance and regulating anaerobic response in plants.		
XX	These are particularly useful in horticultural, agricultural, medical,		
XX	fermentation and cell culture industries. The present sequence is a		
XX	soybean SH2A-like DNA.		
XX	Sequence 889 BP; 270 A; 164 C; 205 G; 250 T; 0 other;		
Query Match 32.8%; Score 285.6; DB 22; Length 889;			
Best Local Similarity 68.3%; Pred. No. 5.6e-78;			
Matches 396; Conservative 0; Mismatches 184; Indels 0; Gaps 0;			

Qy	83	CCAGGATGGTAAAGACGGAGGTGATAGAGCATGGTACATGGATGATAGCAGAGGACCA	142	PR	16-APR-1999;	99US-0129845.
Db	46	CAAGCATCCACGAGAGGATGTCCTTCRAAGCTGGTACATGGATGATAGATCA	105	PR	21-APR-1999;	99US-0130077.
Qy	143	GAGCTTCCTCATCACCGCGAGAACCCAAAGAATTTCATCCCTGTTGATAGCTTACAGAACT	202	PR	23-APR-1999;	99US-0130449.
Db	106	AAGACTCCCCCACCAAAAGAACCCAAAGGATTTGTCTCGTTGGACCAACTTGTGTAAC	165	PR	23-APR-1999;	99US-0130510.
Qy	203	AGGAGTAATCAGCTGGCGCCTAAATCCTGATACTGGGAGAAATTCGCGAGAACCTGAAGAG	262	PR	30-APR-1999;	99US-0130891.
Db	166	TGAGTCTTAGCTGGAAACTAGATGCTGATAACCATGAAATGATCAGAGCTGAAGAA	225	PR	30-APR-1999;	99US-0131449.
Qy	263	AATCCGCGAAGCCAGAGGTACTCTTATGTGGACATTTGTGATGTCGCCAGAGAGCT	322	PR	04-MAY-1999;	99US-0132048.
Db	226	GATTCGTGAAGAGCGTGGTTACACCTACATGGATGTTGTGAGGTCGCCAGAAAAGTT	285	PR	04-MAY-1999;	99US-0132407.
Qy	323	GCCAAATATGAAGCTAAGAGTCTTTTGAAGAAGACACCTGCATACCGATGAAGA	382	PR	05-MAY-1999;	99US-0132484.
Db	286	GCCAAATATGAAGAGAAATCAAAAGCTTCTTTGAAGAGCATCTTCACATGATGAGGA	345	PR	06-MAY-1999;	99US-0132485.
Qy	383	AATACGCTATGCTTGAAGGAGTGGATGATCTTTGATGTGAGAGCAAAAATGATCAGTG	442	PR	06-MAY-1999;	99US-0132486.
Db	346	GATCCGCTTTTGTGCTGCTGAAGTGGCTATTTTGATGTTAGGATCGCAATGAAGCTTG	405	PR	07-MAY-1999;	99US-0132487.
Qy	443	GATTGCTATAGCACTGAAGAAAGGAGGCATGATGTTCTGCTGCAGGGATGTACCAACG	502	PR	11-MAY-1999;	99US-0132863.
Db	406	GATTCGTGTGTGGTCAAGAAAGAGGAAGTATCATCTTACCTGCCGGAATTTATCATCG	465	PR	11-MAY-1999;	99US-0134256.
Qy	503	CTTTACGTTGGACACCGACCAACTATATCAAGGCAATCGACTGTTTCTGCGGATCCTGT	562	PR	14-MAY-1999;	99US-0134218.
Db	466	CTTTACGCTAGATGAGAGCAACTACATTAAGGCTTTCGCTTTTGTGGTGAGCCAGT	525	PR	14-MAY-1999;	99US-0134219.
Qy	563	TTGGACACCTACAAACCGTCCCATGACCATCTTCTGCAAGAAAGGAGTTTTCGGCTAA	622	PR	14-MAY-1999;	99US-0134221.
Db	526	TTGGACTCCATACAATCGTCCAAATGACCATCTCCCTGCRAGACAAATATGTCAGGA	585	PR	14-MAY-1999;	99US-0134370.
Qy	623	ACTTCTCAAGTCAAGAGGTGAAATCAAGCAGTTGAAGGC	662	PR	18-MAY-1999;	99US-0134376.
Db	586	TTTTGTGGAAGAGGATGTTAGCAGCCATGCTGTTGATGCC	625	PR	18-MAY-1999;	99US-0134941.
RESULT 15						
AAC48250						
ID	AAC48250 standard; DNA: 1300 BP.					
XX	AAC48250;					
XX	AAC48250;					
DT	18-OCT-2000 (first entry)					
DE	Arabidopsis thaliana DNA fragment SEQ ID NO: 56805.					
DE	Arabidopsis thaliana.					
XX	OS					
XX	EP1033405-A2.					
XX	06-SEP-2000.					
PD	25-FEB-2000; 2000EP-0301439.					
PPF	25-FEB-1999; 99US-0121825.					
PR	05-MAR-1999; 99US-0123180.					
PR	09-MAR-1999; 99US-0123548.					
PR	23-MAR-1999; 99US-0125788.					
PR	25-MAR-1999; 99US-0126264.					
PR	29-MAR-1999; 99US-0126785.					
PR	01-APR-1999; 99US-0127462.					
PR	06-APR-1999; 99US-0128234.					
PR	08-APR-1999; 99US-0128714.					

Hybridisation assay; genetic mapping; gene expression control;
protein identification; signal transduction pathway;
metabolic pathway; promoter; termination sequence; ss.

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 20:05:08 ; Search time 72 Seconds
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3714.196 Million cell updates/sec

Title: US-09-785-738A-1

Perfect score: 872

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS.COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
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3	172	19.7	1093	4	US-09-348-265-1
4	55.6	6.4	7218	1	US-08-232-463-14
5	33.4	3.8	1323	1	US-08-858-207A-50
6	32.8	3.8	1627	1	US-08-615-170-2
7	32.8	3.8	1666	1	US-08-615-170-4
8	32.2	3.7	7432	1	US-07-852-260-1
9	32.2	3.7	7432	2	US-08-461-503-1
10	32.2	3.7	7432	3	US-08-465-250-1
11	31.8	3.6	3572	2	US-08-713-815A-2
12	31.4	3.6	4325	1	US-08-453-924-2
13	31.4	3.6	4325	1	US-08-471-791-29
14	31.4	3.6	4325	5	PCT-US91-01746-29
15	31.2	3.6	2169	4	US-09-434-408-3
16	30.8	3.5	686	3	US-09-142-514-2
17	30.8	3.5	19307	3	US-08-836-032A-10
18	30.8	3.5	19307	4	US-09-427-048A-10
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Sequence 17, Appli
Sequence 17, Appli
Sequence 1620, Ap
Sequence 14, Appl
Sequence 214, App
Sequence 114, App
Sequence 117, App
Sequence 2, Appli
Sequence 159, App
Sequence 32, Appl
Sequence 3, Appli
Sequence 3, Appli

28 30.2 3.5 1245 4 US-08-961-527-257
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34 30 3.4 289 4 US-09-244-796-17
35 30 3.4 903 4 US-09-134-001C-1620
36 29.8 3.4 2520 4 US-08-961-527-14
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38 29.8 3.4 2560 4 US-08-961-527-114
c 39 29.8 3.4 4327 4 US-08-961-527-117
40 29.8 3.4 7431 4 US-09-306-998-2
41 29.8 3.4 9048 4 US-08-961-527-159
42 29.6 3.4 248 4 US-09-007-005-32
43 29.6 3.4 248 4 US-09-244-796-32
44 29.6 3.4 277 4 US-09-007-005-3
45 29.6 3.4 277 4 US-09-244-796-3

ALIGNMENTS

RESULT 1
US-08-933-750C-77
: Sequence 77, Application US/08933750C
: Patent No. 5932442
: GENERAL INFORMATION:
: APPLICANT: Lal, Preeti
: APPLICANT: Hillman, Jennifer L.
: APPLICANT: Bandman, Olga
: APPLICANT: Shah, Purvi
: APPLICANT: Au-Young, Janice
: APPLICANT: Yue, Henry
: APPLICANT: Guegler, Karl J.
: APPLICANT: Corley, Neil C.
: TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
: NUMBER OF SEQUENCES: 98
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Incyte Pharmaceuticals, Inc.
: STREET: 3174 Porter Drive
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/933,750C
: FILING DATE: September 23, 1997
: CLASSIFICATION: 536
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER:
: FILING DATE:
: ATTORNEY/AGENT INFORMATION:
: NAME: Billings, Lucy J.
: REGISTRATION NUMBER: 36,749
: REFERENCE/DOCKET NUMBER: PF-0356 US
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-855-0555
: TELEFAX: 415-845-4166
: TELEX:
: INFORMATION FOR SEQ ID NO: 77:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1107 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: IMMEDIATE SOURCE:
: LIBRARY: LINDNOT03

CLONE: 1577239
US-08-933-750C-77

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Best Local Similarity 61.7%; Pred. No. 1.2e-52;
Matches 318; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

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DB 108 ACCCGCGCGCCAGTGGCGCTGGAGAGCTGGCGCGCTGGCGCTGGCGCTGGCGAGC 167
QY 223 TAAATCTGTAACTGGGAGAAATTCGAGAACCTGAAGAGAAATCCGCGAGCAGAGGTT 282
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QY 343 TCAAGAGTTCTTTGAGAACACCTGATACCGATGAAGAAATACGCTATGCTTTGAAG 402
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QY 463 AAGGAGCATGATTTGCTGCTGCGAGGATGTACACCGCTTTAGCTTGGACACCGACA 522
DB 408 AGGAGAGATGATGACGCTGCCCGCGGGATCTATCACCGCTTACGCTGGAGGAGAAGA 467
QY 523 ACTATATCAAGCAATGGAGTCTTTGTCGCGATCTGTTGGACACCTTCAACACGCTC 582
DB 468 ACTACAGAGCCATGCGGCTGTTTGTGGAGAACCGGTGTGACAGCGCTACACCGGC 527
QY 583 CCCATGACATCTTCCTGCAAGAAAGAGTTTTTG 617
DB 528 CCGCTGACCATTTTGAAGCCCGCGGAGTACGTG 562

RESULT 2

US-09-234-613-77
; Sequence 77, Application US/09234613
; Patent No. 6132973

GENERAL INFORMATION:

; APPLICANT: Lal, Preeti
; APPLICANT: Hillman, Jennifer L.
; APPLICANT: Bandman, Olga
; APPLICANT: Shah, Purvi
; APPLICANT: Au-Young, Janice
; APPLICANT: Yue, Henry
; APPLICANT: Guegler, Karl J.
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/234,613

; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA: US/08/933,750
; FILING DATE: September 23, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0356 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 77:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1107 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: LMODNOT03
; CLONE: 1577239
; US-09-234-613-77

Query Match 22.9%; Score 199.8; DB 3; Length 1107;
Best Local Similarity 61.7%; Pred. No. 1.2e-52;
Matches 318; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

QY 103 TGATAGAGCATGGTACATGATGATGAGAGAGGAGGCTTCCTCATCAGCGG 162
DB 48 TGGTCAGGCTGTATGATGAGAGCGCCCGCGGACCCGCGCAACCCACCGCCCG 107
QY 163 AACCCAAAGAAATTCATCTCTGATGATAAGCTTACAGAACTAGGAGTAATCAGCTGGCGCC 222
DB 108 ACCCGCGCGCCAGTGGCGCTGGAGCAGTGGCGCGCTGGCGCTGGCGCTGGCGAGC 167
QY 223 TAAATCTGTAACTGGGAGAAATTCGAGAACCTGAAGAAATCCGCGAGCAGAGGTT 282
DB 168 TGGATGCTGACAAATATGAGAAATGATCCAGAAATAGAAAAGATCCGAGAGAGGAACT 227
QY 283 ACTCTATGTGGACATTTGTGATGTGTCGCCAGAGAAAGCTGCCAAATATGAAACTAAGA 342
DB 228 ACTCTGGATGACATCATAACCATATGCAAAAGATNAACTACCAATATGAAGAAAAGA 287
QY 343 TCAAGAGTTCTTTGAGAACACCTGATACCGATGAAGAAATACGCTATGCTTTGAAG 402
DB 288 TTAAGATGTTCTACGAGGAGCATTTGCACTTGGACGATGAGATCCGCTACATCTGGATG 347
QY 403 GGAGTGGATATCTTGTATGATGAGAGACCAAAATGATCAGTGGATTCGTATAGCACTGAAGA 462
DB 348 GCAGTGGTACTTCGAGTGAGGACAAAGGACGACAGTCCGATCCGATCTTCATGAGAGA 407
QY 463 AAGGAGCATGATTTGCTGCTGCGAGGATGTACACCGCTTTAGCTTGGACACCGACA 522
DB 408 AGGAGAGATGATGACGCTGCCCGCGGGATCTATCACCGCTTACGCTGGAGGAGAAGA 467
QY 523 ACTATATCAAGCAATGGAGTCTTTGTCGCGATCTGTTGGACACCTTCAACACGCTC 582
DB 468 ACTACAGAGCCATGCGGCTGTTTGTGGAGAACCGGTGTGACAGCGCTACACCGGC 527
QY 583 CCCATGACATCTTCCTGCAAGAAAGAGTTTTTG 617
DB 528 CCGCTGACCATTTTGAAGCCCGCGGAGTACGTG 562

RESULT 3

US-09-348-265-1
; Sequence 1, Application US/09348265
; Patent No. 644800
; GENERAL INFORMATION:
; APPLICANT: KIKUCHI, Kokiichi
; APPLICANT: SATO, No. 6444800iyuki
; APPLICANT: TORIGOE, Toshihiko

```

; APPLICANT: SAHARA, Hiroeki
; APPLICANT: SUZUKI, Manabu
; APPLICANT: HAMURO, Junji
; TITLE OF INVENTION: Human Gastric Cancer Antigen Gene and Gastric
; TITLE OF INVENTION: Cancer Antigen Protein
; FILE REFERENCE: OP871
; CURRENT APPLICATION NUMBER: US/09/348,265
; CURRENT FILING DATE: 1999-07-07
; EARLIER APPLICATION NUMBER: JP 10-197852
; EARLIER FILING DATE: 1998-07-13
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1093
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (46)..(534)
US-09-348-265-1

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Query Match	19.7%	Score 172;	DB 4;	Length 1093;
Best Local Similarity	61.9%;	Pred. No. 5,8e-44;		
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QY 122	GGATGATCGGAAGAGGACACAGAGGCTTCCTCATCCCGCGAACCCAAAGAAATTCATTCC	181		
Db 67	GGACGACGCCCGGGCGACCGCGGCAACCCACCGCCCGCCAGCCCGGCCCGCCAGTGG	126		
QY 182	TG--TTGATAGCTTTACAGAATAGGAGTAATCAGCTGGCGCTAAATCCTGATAACTGG	239		
Db 127	GCCTTGGAGCAGCTCGCGGCTCTACTTGGNAAGCTGGATCGTGACAAATAT	186		
QY 240	GAGAATTCGGAGACCTTGAAGAGAAATCCGCGAAGCCAGAGGTTACTCTTATGTGGACATT	299		
Db 187	GAGAATGTCCAGAATTAGAAAGATCCGAAGAGAGAGGAATCTACTCTGGATGGACATC	246		
QY 300	TGTGATGTCTCCCGAGAGAACTCCCAAAATTATGAACACTAAGATCAAGAGTTCCTTGA	359		
Db 247	ATAACCATATCGAAGATATAACTTCCAAATATTGAAGAAAGAAATTAAGATGTCTACGAG	306		
QY 360	GAACACCTGCATACCCGATGAAGAATACGCTATTGTCTTGAAGGGATCGATCTTTGAT	419		
Db 307	GAGCATTTGCATCTGGACGATGAGATCCGCTACATCTCGGTGGCASTCGGTACTTCGAC	366		
QY 420	GTGAGAGACCAAAATGATCATGTGGATTCGTATAGCACTGAAGAAGGAGCATGATGTT	479		
Db 367	GTGAGGACAAAGGAGGACCATGTGATCCGGATCTTCATGTGAGAAGGAGACATGGTGACG	426		
QY 480	CTGCCTGCAGGGATGTACCCCGCTTTACGTTGGACACCGACAACTATATCAAGSCAATG	539		
Db 427	CTCCCCCGGGGATCTATCAACCGTTTCCCGTGTGACGAGAAGAACTACACGAAGGCCATG	486		
QY 540	CGAC-TGTTTGTGGCGATCTCTGTTTGGACACCCCTACAACCGTCCCATGACCATCTCC	598		
Db 487	CGSGTGTGTTGGGAGAAACCGGTCTGACCGGTTGACGAGAAGAACTACACGAAGGCCATG	546		
QY 599	TGCAAGAAGGAGT	612		
Db 547	AGCCCGCGGGAGT	560		

RESULT 4
US-08-232-463-14/c
; Sequence 14, Application US/08232463
; Patent No. 5670367

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: GENERAL INFORMATION:
: APPLICANT: DORNER, F.
: APPLICANT: SCHEIFELINGER, F.
: APPLICANT: FALKNER, F. G.
: TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
: NUMBER OF SEQUENCES: 52
: CORRESPONDENCE ADDRESS:
:

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ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232.463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935.313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: ptzqpt-Fls
US-08-232-463-14

Query Match	6.4%; Score 55.6; DB 1; Length 7218;
Best Local Similarity	8.4%; Pred. No.3e-07;
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QY	115 GGTCATCGATGATAGCGAAGAGACCAGACTTCCTCATTACCGCGAACCCACAAGAT 174 :
Db	1417 RRR 1958 :
QY	175 TCATTCTGTGTATAAGCTTACAGAACATAGGAGTAATCAGCTGGCGCCTAAATCCTGATA 234 :
Db	1357 RRR 1298 :
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Db	1297 RRR 1238 :
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Db	1237 RRR 1178 :
QY	355 TTGAAGACACCTGCATACCGATGAAGAAATACGCTATTGCTGAAGGGAGTGCATFACT 414 :
Db	1177 RRR 1118 :
QY	415 TTCATGTGAGACCAAAAATGATCAGTGATCGTATAGCACTGAAGAAAGAGCGCATGA 474 :
Db	1117 RRR 1058 :
QY	475 TTGTTCTGCCTGCAGGGATG 494
Db	1057 TCCCTCGACCTGCAGCCAAG 1038


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RESULT 8
US-07-852-260-1
; Sequence 1, Application US/07852260
; Patent No. 5525715
; GENERAL INFORMATION:
; APPLICANT: RacanIELlo, Vincent
; APPLICANT: Tatem, Joanne M.
; APPLICANT: Weeks-Levy, Carolyn L.
; TITLE OF INVENTION: METHODS FOR PRODUCING RNA VIRUSES FROM
; TITLE OF INVENTION: CDNA
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA: US/07/852.260
; APPLICATION NUMBER:
; FILING DATE: 19920619
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 36607-B-PCT-US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 977-9550
; TELEFAX: (212) 664-0525
; TELEX: 422523 COOP UI
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7432 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 743..7361
; US-07-852-260-1

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Best Local Similarity 47.3%; Pred. No. 6.2;
Matches 97; Conservative 0; Mismatches 108; Indels

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Qy 318 AAGCTGCCAAAATTATGAAACTAAGATCAAGAGCTTTCTTTTGAAGAACAACCTGCATC
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Qy 378 GAAGAAATACGCTATTGTCTTTGAAGGGAGTGGATACTTTTGTATGTGTAGAGACCA
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Db 6161 TATGTAGGGAACAAGATCATCACTGAGGTGATGATGATGATAAGAAAGAGGCAGTGGAC

Qy 438 CAGTGGATTTCGTATAGCACTGAAGA 462
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Db 6221 CTGGCAACATTATGCTCGCTGGATA 6245

RESULT 9
US-08-461-503-1

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1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: 07/550,804
3 FILING DATE: 09-JULY-1990
4 PRIOR APPLICATION DATA:
5 APPLICATION NUMBER: 07/147,781
6 FILING DATE: 25-JANUARY-1988
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: 07/078,538
9 FILING DATE: 28-JULY-1987
10 PRIOR APPLICATION DATA:
11 APPLICATION NUMBER: 06/891,529
12 FILING DATE: 31-JULY-1986
13 ATTORNEY/AGENT INFORMATION:
14 NAME: Rae-Venter, Barbara
15 REGISTRATION NUMBER: 32,750
16 REFERENCE/DOCKET NUMBER: CGNE-037/04US
17 TELECOMMUNICATION INFORMATION:
18 TELEPHONE: (415) 926-6200
19 TELEFAX: (415) 854-3713
20 INFORMATION FOR SEQ ID NO: 2:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 4325 base pairs
23 TYPE: nucleic acid
24 STRANDEDNESS: both
25 TOPOLOGY: linear
26 MOLECULE TYPE: DNA (genomic)
27 FRAGMENT TYPE: linear
28 FEATURE:
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30 NAME/KEY: CDS
31 LOCATION: 2152..2703
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33 US-08-453-924-2
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35 Query Match 3.6%; Score 31.4; DB 1; Length 4325;
36 Best Local Similarity 64.4%; Pred. No. 8.5;
37 Matches 47; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
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39 QY 44 CTCCTGCTTCACCCGCAATCCACATGGAGACGAAATCCACAGATGGTAAGACCGAGGT 103
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41 Db 4234 CCCTACTTCAATGCCCAATCTACTTGGAAACACAGACACAGATGGGAAAGTTGATGA 4293
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43 QY 104 GATGAAGACATGG 116
44 ||| |||| ||||
45 Db 4294 GATCCAAGCTTGG 4306
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47 RESULT 13
48 US-08-471-791-29
49 Sequence 29, Application US/08471791
50 Patent No. 5723595
51 GENERAL INFORMATION:
52 APPLICANT: Thompson, Gregory A
53 APPLICANT: Knauf, Vic C
54 TITLE OF INVENTION: Plant Desaturases-Compositions
55 TITLE OF INVENTION: and Uses
56 NUMBER OF SEQUENCES: 45
57 CORRESPONDENCE ADDRESS:
58 ADDRESSEE: Calgene, Inc.
59 STREET: 1920 Fifth Street
60 CITY: Davis
61 STATE: California
62 COUNTRY: USA
63 ZIP: 95616
64
65 COMPUTER READABLE FORM:
66 MEDIUM TYPE: diskette, 3.50 inch, 2.0 MB storage
67 COMPUTER: Apple Macintosh
68 OPERATING SYSTEM: Macintosh 7.1
69 SOFTWARE: MicrosoftWord 5.1 (a)
70 CURRENT APPLICATION DATA:
71 APPLICATION NUMBER: US/08/471,791
72 FILING DATE: 6-JUNE-95
73 CLASSIFICATION: 435
74 PRIOR APPLICATION DATA:
75 APPLICATION NUMBER: 07/762,762

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ob time : 116 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

3M nucleic - nucleic search, using sw model

Run on: December 1, 2002, 21:04:18 ; Search time 105 Seconds
(without alignments)

3198.292 Million cell updates/sec

Title: US-09-785-738A-1

Perfect score: 872
Sequence: 1 agacgaacacacacagaat.....acaggagtcagtgaagctgaa 872

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 341543 seqs, 192557720 residues

Total number of hits satisfying chosen parameters: 683086

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications NA:
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2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq.*
3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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3	339.2	38.9	933	10	US-09-785-738A-11
4	311.8	35.8	774	10	US-09-785-738A-5
5	307	35.2	849	10	US-09-770-445-629
6	285.6	32.8	889	10	US-09-785-738A-9
7	244	28.0	743	10	US-09-770-149-44
8	242	27.8	603	10	US-09-785-738A-7
9	213	24.4	2823	9	US-09-938-842A-1843
10	207.8	23.8	972	10	US-09-785-738A-15
11	201	23.1	1176	10	US-09-945-301-545
12	199.8	22.9	1107	10	US-09-840-787-77
13	182.8	21.0	403	10	US-09-878-574-3886
14	182.4	20.9	706	10	US-09-785-738A-17
15	181.8	20.8	920	10	US-09-785-738A-13
16	172	19.7	1093	9	US-10-191-322-1
17	154.8	17.8	456	10	US-09-880-107-1349
18	136.8	15.7	300	9	US-09-964-899-36
19	123.8	14.2	267	10	US-09-923-876-5392

ALIGNMENTS

RESULT 1

US-09-785-738A-1

; Sequence 1, Application US/09785738A

; Patent No. US2002032918A1

; GENERAL INFORMATION:

; APPLICANT: Sauter, Margret M

; APPLICANT: Lorbiecke, Rene

; TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC

; FILE REFERENCE: 2283/201

; CURRENT APPLICATION NUMBER: US/09/785,738A

; PRIOR FILING DATE: 2001-02-16

; PRIOR FILING DATE: 2000-02-18

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 872

; TYPE: DNA

; ORGANISM: Rice

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (69)..(668)

US-09-785-738A-1

Query Match 100.0%; Score 872; DB 10; Length 872;
Best Local Similarity 100.0%; Pred. No. 3.2e+252;
Matches 872; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 CAATCCACATGGAGACGAAATTCAGGATGTTAAGACGGAGGTGATAGAACGATGGTACA 120

Db 61 CAATCCACATGGAGACGAAATTCAGGATGTTAAGACGGAGGTGATAGAACGATGGTACA 120

Qy 121 TGGATGATAGCGAAGAGGACGAGGCTTCCTCATCCCGGACCCAAAGAAATTCATTC 180

Db 121 TGGATGATAGCGAAGAGGACGAGGCTTCCTCATCCCGGACCCAAAGAAATTCATTC 180

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Sequence 6162, Ap
Sequence 174, App
Sequence 5315, Ap
Sequence 14604, A
Sequence 81, Appl
Sequence 12507, A
Sequence 6204, Ap
Sequence 14619, A
Sequence 4750, Ap
Sequence 41, Appl
Sequence 1, Appl
Sequence 1, Appl
Sequence 1965, Ap
Sequence 6, Appl
Sequence 9, Appl
Sequence 13768, A
Sequence 611, App
Sequence 342, App
Sequence 3897, Ap
Sequence 298, App
Sequence 9803, Ap
Sequence 898, App
Sequence 248, App
Sequence 8596, Ap

20 100.6 11.5 274 10 US-09-923-876-6162
21 98.6 11.3 263 10 US-09-923-876-174
22 95.8 11.0 312 10 US-09-878-574-5315
23 86.4 9.9 232 10 US-09-960-352-14604
24 83.4 9.6 386 10 US-09-770-791-81
25 82.6 9.5 259 10 US-09-878-574-12507
26 80.2 9.2 242 10 US-09-878-574-6204
27 46.2 5.3 358 10 US-09-960-352-14619
28 38 4.4 2000 9 US-09-938-842A-4750
29 36 4.1 900 10 US-09-861-451A-41
30 35.2 4.0 1503841 9 US-09-946-807-1
31 35.2 4.0 1503841 10 US-09-795-668-1
32 35.2 4.0 1503841 10 US-09-795-686-1
33 32.4 3.7 26197 10 US-09-764-847-1965
34 31.8 3.6 180557 12 US-10-003-806-6
35 31.8 3.6 180557 12 US-10-003-806-9
36 31.6 3.6 581 10 US-09-864-761-13768
37 31.6 3.6 581 10 US-09-864-761-30307
38 31.6 3.6 4389 12 US-10-044-090-611
39 31.6 3.6 4531 10 US-09-925-300-342
40 31.6 3.6 28897 10 US-09-764-877-3897
41 31.4 3.6 545 10 US-09-815-343-298
42 31.4 3.6 2706 10 US-09-815-242-9803
43 31 3.6 531 10 US-09-917-800A-898
44 31 3.6 644 10 US-09-917-800A-248
45 30.8 3.5 234 10 US-09-878-574-8596

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QY 241 AGAATGGGAGAACTGAGAGAAATCCGGAAGCCAGAGGTACTCTTATGTGGACATTT 300
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QY 481 TGCCCTGAGGAGTACCAACCGCTTAGCTTGGACACCGACCACTATATCAAGGCAATGC 540
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QY 601 CRAAGAGAGTGTGCTAACTTCTCAGTCAGAGTGGAAGTGAAGTGAAG 660
Db 601 CRAAGAGAGTGTGCTAACTTCTCAGTCAGAGTGGAAGTGAAGTGAAG 660
QY 661 GCTTCTGAGGGTTTCTTGGGCTCCTGCACTGCGGTTCTATATCAACCTGAAATAGATG 720
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QY 781 AGATTTAATGATTTTCTTAACTTATGATCAATCGGCATATAGCACTTCGGAATG 840
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QY 841 TGTTTTCATAACAGGAGTATGAAGCTGAA 872
Db 841 TGTTTTCATAACAGGAGTATGAAGCTGAA 872
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RESULT 2
US-09-785-738A-3
; Sequence 3, Application US/09785738A
; Patent No. US20020032918A1
; GENERAL INFORMATION:
; APPLICANT: Sauter, Margret M
; APPLICANT: Lorbiecke, Rene
; TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
; FILE REFERENCE: 2283/201
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,572
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 980
; TYPE: DNA
; ORGANISM: Rice
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (139)..(735)
US-09-785-738A-3
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Query Match 48.7%; Score 424.4; DB 10; Length 980;
Best Local Similarity 83.3%; Pred. No. 1.1e-117;
Matches 495; Conservative 0; Mismatches 96; Indels 3; Gaps 1;

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Db 137 AGATGAGAACCACTTCCAGAGTGGCAAGGAGGAGGTGATGAAAGCTGGTACATGATG 196
QY 127 ATAGCGAAGAGGAGGAGGCTTCCTCATCACCAGCAACCAAGAAATTCATTCCTGTTG 186
Db 197 ACATGAGAACGAATTCAGAGTGTGAACACGAGGTGATAGAACCATGGTACATGATG 256
QY 187 ATAGCTTACAGAACTAGGAGTAACTAGCTGGCGCTTAATCTCTGATGAATGAGGAAAT 246
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QY 307 TGTCGCCAGAGAGCTGCCAAATATGAAACTTAAGATCAAGAGTTTCTTTGAAGAACACC 366
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QY 367 TGCACTACCGATGAAGAAATACGCTATTGCTTGAAGGAGTGGATACCTTTCATGTGAGAG 426
Db 437 TGCACTACCGATGAAGAGATACGCTATTGCTTGAAGGAGTGGATACCTTTCATGTGAGAG 496
QY 427 ACCAAATGATCAGTGGATTCGTATAGCACTGAAGAAAGGAGGCAATGTTCTTCTGCGCTG 486
Db 497 ACCAAATGATCAGTGGATTCGTATAGCACTGAAGAAAGGAGGCAATGTTCTTCTGCGCTG 556
QY 487 CAGGAGTGTACCAACCGCTTTAGCTTGGACACCGCAACTATATCAAGGCAATGCGACTGT 546
Db 557 CAGGAGTGTATCAACCGCTTCACATTTGGACAGTGAACAATACATCAAGGCAATGCGGCTCT 616
QY 547 TTGTTGGCGATCTGTTTGGACACCGCTAGACCGTCCCATGACCATCTTCTCTCAAGAA 606
Db 617 TTGTTGGAGAGCTGTCTGGAGCGCTACACACCGTCCCATGACCATCTGCGAGTAGAA 676
QY 607 AGAGTGTGTTGGTAACTTCTCAAGTCAGAAGGTGAAATCAAGCAGTTTGAAG 660
Db 677 AGAGTGTGTTGGTAACTTCTCAAGTCAGAAGGTGAAATCAAGCAGTTTGAAG 727
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RESULT 3
US-09-785-738A-11
; Sequence 11, Application US/09785738A
; Patent No. US20020032918A1
; GENERAL INFORMATION:
; APPLICANT: Sauter, Margret M
; APPLICANT: Lorbiecke, Rene
; TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
; FILE REFERENCE: 2283/201
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,572
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 933
; TYPE: DNA
; ORGANISM: Cotton
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (33)..(635)
US-09-785-738A-11

Query Match 38.9%; Score 339.2; DB 10; Length 933;
Best Local Similarity 74.8%; Pred. No. 4.2e-92;
Matches 425; Conservative 0; Mismatches 143; Indels 0; Gaps 0
```


[illegible]

```

RESULT 4
US-09-785-738A-5
; Sequence 5, Application US/09785738A
; Patent No. US20020032918A1
; GENERAL INFORMATION:
; APPLICANT: Sauter, Margret M
; APPLICANT: Lorblicke, Rene
; TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 2283/201
; CURRENT APPLICATION NUMBER: US/09/785,738A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,572
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 5
; LENGTH: 774
; TYPE: DNA
; ORGANISM: Tomato
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(591)
US-09-785-738A-5

Query Match          35.8%;   Score 311.8;   DB 10;   Length 774;
Best Local Similarity 72.1%;   Pred. No. 6.5e+84;
Matches 406; Conservative    0; Mismatches 157; Indels    0; Gaps
                                ||| |
Qy      98 GGAGGTGATAGAAGCATTGGTACATGGTAGTCAGCGAAGACCAGAGGCTTCCTCATCA 157

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Db	18	GGATGTCATACAGGCATGGTACATGATGACACACGATGAGGACCAGAGCGCTTCTTCATCA	77
Qy	158	CCGCGAACCCAAAGAATTCAATTCCTGTTGATGAAGCTTACAGAACTAGGAGTAATCAGCTG	217
Db	78	CCGTGAGCCAAAGAAATTTGCTGTCCTTGACAAGCTGGCTGAACTTGGAGTGCTCAGCTG	137
Qy	218	GCGGCTAAATCCTGATAACTGGGAGAAATTCGGGNAACCTTGAGAGAAATCCGCGGAAGCCAG	277
Db	138	GAGACTTGATGCTGACAATTTATGAGACTGATGAGGAGTTTCAAGAAATTCGGGAAGATCG	197
Qy	278	AGGTTACTCTTATGTGGACATTTTGATGTGTGCCAGAGAAAGCTGCCAAATATATGAAC	337
Db	198	TGATATTCAATCATGATTCTGTGAGGTTGCCCTGAGAACTACCGAATACGAGA	257
Qy	338	TAAGATCAAGAGTTCTTTGGAAGACACCTGCATACCGATGAGAAATACGCTATTGCT	397
Db	258	GAATAACAAGAACTTTTGAAGAACACCTGCACACGACGAGGAGATCCGTACGCTGT	317
Qy	398	TGANGGAGTGGTACTTTTCATGTGAGAGACCAAAATGATCAGTGATTCGTTATAGCACT	457
Db	318	TGCAGGAAGTGGTTACTTTTGATGTCGCGGATGTGAATGAGAGCTGGATTCCGGCTGGGT	377
Qy	458	GAAGAAAGGAGGCATGATTCTTGCTGCTGAGGAGTGTACACCGCTTTACGTTTGSACAC	517
Db	378	AAAGAAAGTGGATGATTCTTCTCTGCTGGAATCTATCACCGCTTCCAGCTTGATTC	437
Qy	518	CGACAACATATACAAGCCAAATGGGACTGTFTTGTGGCGATCTCTGTTTGGACACCCCTACAA	577
Db	438	AAGCACTACATTAAGCAATGCGCTCTCTTTGTTGGTGACCCAAATTTGGACTCCATACAA	497
Qy	578	CCGTGCCCATGACCATTCTCTGCAAGAAAGAGTTTGGCTAAACTTCTCAAGTCAGA	637
Db	498	TCGTCCACATGATCATCTCCCGCAGGCAAGAAATATGTTGAGACGCTTGTCAACGCAGA	557
Qy	638	AGGTGAAAATCAACGCTTTGAAG	660
Db	558	TGGCGCTGGTCGTCTGTAAATG	580

```

RESULT 5
US-09-770-445-629/c
; Sequence 629, Application US/09770445
; Patent NO. US20020023281A1
; GENERAL INFORMATION:
; APPLICANT: Goriach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Matthew, Abraham V.
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; FILE OF INVENTION: thaliana
; FILE REFERENCE: 20230US (PARA-012PRV)
; CURRENT APPLICATION NUMBER: US/09/770,445
; CURRENT FILING DATE: 2001-01-26
; PRIOR APPLICATION NUMBER: US 60/178,472
; PRIOR FILING DATE: 2000-01-27
; NUMBER OF SEQ ID NOS: 999
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 629

```

```
; LENGTH: 849
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(849)
; OTHER INFORMATION: n = A,T,C or G
US-09-770-445-629

Query Match          35.2%; Score 307; DB 10; Length 849;
Best Local Similarity 72.4%; Pred. No. 1.9e-82;
Matches 391; Conservative 0; Mismatches 149; Indels 0; Gaps 0;

QY 83 CCAGATGGTAAAGCGAGGTGATAGAGCATGGTACATGGATGATAGGCAAGAGACCA 142
Db 849 CAAGGATGGGAGAGAGAGAGTTCAGGTTGGTATATGATGATAGTCAAGAGATCA 790

QY 143 GAGGCTTCCTCATCACCAGCAACCAAGAAATTCATTCCTGTTGATAAGCTTACAGAACT 202
Db 789 GAGACTTCTCACCACAGGATCCTAAGAGCTTGTATCGTTGGCAAACTTCCAGAGCT 730

QY 203 AGGAGTAATCAGCTGGCGCCCTAAATCCTGATACTGGGAGAAATTCGCAAGAACTTGAAGAG 262
Db 729 GGGAGTACTTACCTGGAGACTTGATGCTGATACCTAGCAAAACCATGAGGATTTGAAAAA 670

QY 263 ANTCCGCGAAGCCAGAGCTTACTCTTATGTGGACATTTGTGATGTGTCGCCAGAGAGCT 322
Db 669 GATCCGTAATCTCGTGTGTACTCTTACATGGAGCTTTGTGAGGTATGCCCGGAAAGCT 610

QY 323 GCCAATATGAACTAAGATCAAGAGTTCTTTTGAAGAACACCTGCATACCGATGAAGA 382
Db 609 TCCAAACTATGAAGTGAAGTAAAGAGCTTTTCGAAGAACATTTGCATACATGATGAAGA 550

QY 383 AATACGCTATTGCTTGAAGGAGTGGATCTTGTGAGCATTTGTGATGTGAGACCAAAATGATCAGTG 442
Db 549 GATCCGTTACTGCTGTGAGGAGTGGTACTTTGATGTGAGAGATCGCAATGAAGCTTG 490

QY 443 GATTCGTATAGCACTGAAGAAGGAGGCATGATTTCTGCTCGCAGGAGTGTACCAACCG 502
Db 489 GATTAGGCTATGGGTAAANNNNAGCTATGATANNNTTACCTGCTGGGATCTATCATCG 430

QY 503 CTTTACGTTGACACCGACACTATATCAAGGCAATCGGACTGTTTGTGGCGATCCTGT 562
Db 429 CTTACCGTGGACTCTGACAACTATATCAAGGCAATCGGCTTTTCGGGTGAACCGGT 370

QY 563 TTGGACACCTTACACCCGTCGCCATGACCATCTTCTGCAAGAAAGAGTTTTTGGCTAA 622
Db 369 ATGGACACCATACAATCGCCACACAGACCATCTTCTGCAAGGAAAGATATGTCGATAA 310

RESULT 6
US-09-785-738a-9
; Sequence 9, Application US/09785738a
; Patent No. US2002032918A1
; GENERAL INFORMATION:
; APPLICANT: Sauter, Margaret M
; APPLICANT: Lorbiecke, Rene
; TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
; FILE REFERENCE: 2283/201
; CURRENT APPLICATION NUMBER: US/09/785,738A
; CURRENT FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: 60/183,572
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 9
; LENGTH: 889
; TYPE: DNA
; ORGANISM: Soybean
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (32)...(634)
```

```
US-09-785-738a-9

Query Match          32.8%; Score 285.6; DB 10; Length 889;
Best Local Similarity 68.3%; Pred. No. 5.2e-76;
Matches 396; Conservative 0; Mismatches 184; Indels 0; Gaps 0;

QY 83 CCAGATGGTAAAGCGAGGTGATAGAGCATGGTACATGGATGATAGGCAAGAGACCA 142
Db 46 CAAGATGCCACGAGAGAGTCTCCTTCAAGCCTGGTACATGGATGATAGTCAAGATCA 105

QY 143 GAGGCTTCCTCATCACCAGCAACCAAGAAATTCATTCCTGTTGATAAGCTTACAGAACT 202
Db 106 AGACTCCCCACCAACAAGAACCCCAAGGAGTTTGTCTGTTGGACCAACTTGTGAACCT 165

QY 203 AGGAGTAATCAGCTGGCGCTTAAATCCTGATACTGGGAGAAATTCGCAAGAACTTGAAGAG 262
Db 166 TGGAGTCTTGTAGCTGGAACCTAGATCTGATAACCATGAAATGATCCAGAGCTGAAGAA 225

QY 263 ANTCCGCGAAGCCAGAGGTACTCTTATGTGGACATTTGTGATGTGTCGCCAGAGAGCT 322
Db 226 GATTCGTTGAAGCGCTGTACACCTTACATGGATGTTGTGTAGGCTTCCCAATGAAGCTTG 285

QY 323 GCCAATATGAACTAAGATCAAGAGTTCTTTTGAAGAACACCTGCATACCGATGAAGA 382
Db 286 GCCAATATGAACTAAGATCAAGAGTTCTTTTGAAGAGCATCTTCACACTGATGAGGA 345

QY 383 AATACGCTATTGCTTGAAGGAGTGGATCTTGTGATGTGAGACCAAAATGATCAGTG 442
Db 346 GATCCGCTTTTGTGCTGCTGGAAGTGGCTATTTGTATGTAGGATTCGAATGAAGCTTG 405

QY 443 GATTCGTATAGCACTGAAGAAGGAGGCATGATTTCTGCTCGCAGGAGTGTACCAACCG 502
Db 406 GATTCGTGTGCTGGTCAAGAAAGGAGGATGATCATCTTACCTGCCGGAATTTATATCG 465

QY 503 CTTTACGTTGACACCGACCAACTATATCAAGGCAATGGAGCTGTTTGTGGCGATCCTGT 562
Db 466 CTTTACGCTAGTGTGAGAGCAACTACATTAAGGCTTTGGCTTTTGTGTGAGGCCAGT 525

QY 563 TTGGACACCTTACACCCGTCGCCATGACCATCTTCTGCAAGAAAGAGTTTTTGGCTAA 622
Db 526 TTGSACTCCATACAATCGTCCAAATGACCATCTCCTGCAAGACAACTATATGTCAGGA 585

QY 623 ACTTCTCAAGTCAGAGGTGAAATCAACGACCTTGAAGGC 662
Db 586 TTTTGTGGAAGAGATGTTAGCAGCCATCTGTGTATGCC 625

RESULT 7
US-09-770-149-44
; Sequence 44, Application US/09770149
; Patent No. US2002005963A1
; GENERAL INFORMATION:
; APPLICANT: Gorlach, Jorn
; APPLICANT: An, Yong-Qiang
; APPLICANT: Hamilton, Carol M.
; APPLICANT: Price, Jennifer L.
; APPLICANT: Raines, Tracy M.
; APPLICANT: Yu, Yang
; APPLICANT: Rameaka, Joshua G.
; APPLICANT: Page, Amy
; APPLICANT: Ledford, Brooke L.
; APPLICANT: Woessner, Jeffrey P.
; APPLICANT: Haas, William David
; APPLICANT: Garcia, Carlos A.
; APPLICANT: Kricker, Maja
; APPLICANT: Slader, Ted
; APPLICANT: Davis, Keith R.
; APPLICANT: Allen, Keith
; APPLICANT: Hoffman, Neil
; APPLICANT: Hurban, Patrick
; TITLE OF INVENTION: Expressed Sequences of Arabidopsis
; LOCATION: thaliana
```

Query Match 27.8%; Score 242; DB 10; Length 603;
Best Local Similarity 65.2%; Pred. NO. 5.4e-63;
Matches 356; Conservative 0; Mismatches 190; Indels 0; Caps

Query Match 28.0%; Score 244; DB 10; Length 743;
Best Local Similarity 67.1%; Pred. No. 1.5e-63;
Matches 346; Conservative 0; Mismatches 170; Indels 0; Gaps 0;

[illegible]

RESULT 8
 US-09-785-738A-7
 ; Sequence 7, Application US/09785738A
 ; Patent No. US20020032918A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sauter, Margret M
 ; APPLICANT: Lorblecke, Rene
 ; TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
 ; TITLE OF INVENTION: CONDITIONS
 ; FILE REFERENCE: 2283/201
 ; CURRENT APPLICATION NUMBER: US/09/785,738A
 ; CURRENT FILING DATE: 2001-02-16
 ; PRIOR APPLICATION NUMBER: 60/183,572
 ; PRIOR FILING DATE: 2000-02-18
 ; NUMBER OF SEQ ID NOS: 18
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 7
 ; LENGTH: 603
 ; TYPE: DNA

```
; LENGTH: 2823
; TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-938-842A-1843

Query Match      24.4%; Score 213; DB 9; Length 2823;
Best Local Similarity 62.8%; Pred. No. 6.1e-54;
Matches 400; Conservative 0; Mismatches 150; Indels 87; Gaps 1;

QY 69 ATGGAGACGAATTCAGAGTGGTAAGACGAGGTGATAGAACATGGTACATGGATGAT 128
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 ATGGGTGAAGCGGTCAAGGATGGGAGAGAGAGTATTCAGCTTGGTATATGGATGAT 60

QY 129 ACGAAGAGACGAGCTTCCATCATCCCGGAGACCCAAAGAAATTCATCTCGTTGAT 188
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 61 AGTGAAGAGATCAGAGACTTCCACACACAGGATCCTAAGAGTTGTATCGTTGGAC 120

QY 189 AAGCTTACAGAACTAGGAGTAAATCAGCTGGCGCTAAATCCTGATACTGGGAGAAATGC 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 121 AAACCTGCAGAGCTGGGAGTACTTAGCTGGAGACTTGATGCTGATACATGAACCCGAT 180

QY 249 GAGAACCTGAAGAGAAATCCGCGAAGCCAGAGGTTACTCTTATCT 292
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 181 GAGGATTTGAAAAGATCCGTTGAATCTCGTGGTTACTCTTCATGTTGTGTTTAT 240

QY 293 ----- 292
Db 241 TTATTACTATCCCACTAGACTTGAATGGTAGATGTTATTATTTGTCCAAGTCTTATTT 300

QY 293 -----GGACATTTGATGTGTGCCAGAGAGCTGCCAAATTAAGAACTAAG 341
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 301 AACTCTTAGGGACTTTTGTGAGTATGCCGGAAGATTCACAACTATGAAGTGAA 360

QY 342 ATCAAGAGTTCTTTGAAGACACCTGCATACCGATGAAGAAATACGCTATTGCTTGAA 401
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 361 GTGAAGAGCTTTTCGAAGACATTTACACACTGATGAGGAGATCCGTTACTGCTTGA 420

QY 402 GGGAGTGATCTTTGATGTGAGAGACCAAAATGATCAGTGGATTCGTATACACTGAAG 461
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 421 GGAATGTTACTTTGATGTGAGAGATCGTAAGAAGCTTGGATAGGATATGGTAAAG 480

QY 462 AAAGGAGCATGATTTCTTCCTCCAGGATGTACACCGCTTTACGTTGGACACCGAC 521
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 481 AAGGGAGGTATGATAGTCTTACCTGCTGGGATCTATCATCGCTTCACTGGGACTCTGAC 540

QY 522 AACTATATCAAGCAATCGGACTGTTCTTGGCGATCCTGTTTGGACACCCCTACACCGT 581
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 541 AACTATATCAAGCAATCGGCTATTCTGTTGGTGAACCGGTATGGACACCATACAATCCG 600

QY 582 CCCATGACCATCTTCTCGCAAGAAAGAGTTTGTG 618
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 601 CCACAGCACCATCTTCTCGCAAGAGTGTCTGTTGG 637
```

```
RESULT 10
US-09-785-738A-15
; Sequence 15, Application US/09785738A
; Patent No. US20020032918A1
; GENERAL INFORMATION:
; APPLICANT: Sauter, Margret M
; APPLICANT: Lorbiecke, Rene
; TITLE OF INVENTION: ALTERATION OF GROWTH AND ADAPTATION UNDER HYPOXIC
; FILE REFERENCE: 2283/201
; CURRENT APPLICATION NUMBER: US/09/785,738A
; CURRENT FILING DATE: 2001-02-16
; PRIOR FILING DATE: 2000-02-18
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 15
; LENGTH: 972
; TYPE: DNA
```

```
; ORGANISM: Mouse
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (37)..(556)
US-09-785-738A-15

Query Match      23.8%; Score 207.8; DB 10; Length 972;
Best Local Similarity 63.5%; Pred. No. 1.3e-52;
Matches 317; Conservative 0; Mismatches 182; Indels 0; Gaps 0;

QY 103 TGATAGAAGCATGGTACATGGATAGTAGAGAGGACGAGAGGCTTCTCATCACCGCG 162
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 18 TGGTCAGCGCTGTTATATGGAGAGTCCACGCGCGACCCGCGGAAGCCACCGCGCAC 77

QY 163 AACCCAAAGNAATTCATCTCTGTGTATAGACTTACAGAACTAGGAGTAACTAGCTGGCGCC 222
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 78 AGCCCGACCGCCCGTGGAGCTTGGAGCAGCTGCGCACCTCGGAGTGTCTTATTGGAAGC 137

QY 223 TAAATCCTGATTAATCTGGGAAATTCGAGAACCTGAAGAGAAATCCGGAAGCCAGAGGTT 282
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 138 TAGATGCTGACAAAGTATGAGAACGATCCAGAACTAGAAAAGATCCGGAATAATGAGAACT 197

QY 283 ACTCTTATGTGGACATTTGTGATGTGTGCCAGAGAACTGCCAAATTAAGAACTAAGA 342
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 198 ACTCTTGGATGGGACATCATCACCATATGCAAGATACACTTCCCAATTTACGAGGAGA 257

QY 343 TCAAGAGTTTCTTTGAAGAACACCTGCATACCGATGAAGAAATACGCTATTGTTGAAG 402
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 258 TCAAGATGTTCTTTGAGGAACATCTGCATCTGGATGAGGAGATCCGCTTACATCTCGAGG 317

QY 403 GGAGTGGATACATTTGATGTGACAGACCAAAATGATCAGTGGATTCGTATAGCACTGA 462
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 318 GTAGTGGTACTTCGATGTGACAGGACAAGGAGCAAGTGGATTCGGATTTCCATGAGA 377

QY 463 AAGGAGCATGATTTGTTCTGCTGCGAGGATGTACCCGCTTTACGTTGGACACCGACA 522
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 378 AGGGGACATGATTACTCTCTCCGCGCATCTATCACCGCTTCACACTGAGCAGAGA 437

QY 523 ACTATATCAAGCAATGCGACTGTTGTTGGCGATCCTGTTTGGACACCCCTACACCGTC 582
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 438 ATTACGTGAAGGCAATCGCGCTGTTTGTGGAGAACCTGTGTGGACACCATACAACCGC 497

QY 583 CCCATGACCATCTTCTCTGC 601
    ||| ||| ||| ||| |||
Db 498 CAGCTGACCATTTTGATGC 516
```

```
RESULT 11
US-09-925-301-545
; Sequence 545, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR FILING DATE: PCT/JUS00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 545
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-301-545

Query Match      23.1%; Score 201; DB 10; Length 1176;
Best Local Similarity 61.7%; Pred. No. 1.6e-50;
Matches 318; Conservative 1; Mismatches 196; Indels 0; Gaps 0;
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103	TCATAGAGCATGCTACATGATGATAGCGAAGAGCCAGGAGCTTCTTCATCACGGC	166
111		
83	TGTGTGAGGCTTGGTATATGAGCAGCGCCCGGGCGCCGCGCAACCCACCGCCCGC	142
163	AACCCAAAGAATTCAATTCCTGTGTGATAAGCTTACAGAACTAGGAGTAATCAGCTTGGGGCC	222
143	ACCCGGCGCCGCCAGTGGGGCTTGGACAGCTCGCGGCGCTCGGGGTGCTCTACTTGAAGC	202
223	TAAATCCTGATAACTGGGAGAAATTGGCAGAACTCTGAAGAAATCCGCGAAGCCAGAGAGTT	282
203	TGCATGCTGACAAATATACGAATGATCCAGAATTAGAAAAGTCCGAAGAGAGAGGAACT	262
283	ACTCTTATGTGACAAATTTGTGATGTGTGCCAGAGAGAGCTGCCAAATATTGAAACTAAGA	342
263	ACTCTCGATGACATCATTAACCATATGCAAGATTAACCTACCAATTTATGAGAAAGA	322
343	TCAGAGATTTCTTTGAAGAACACCTCGCATACCGATGAAGAAATAGCTTATTTGCTTGAAG	402
323	TTAAGATCTTCTACGAGGAGCATTTGCATCTTGACGAGATCAGATCCGCTACATCCTGGATG	382
403	GGAGTGGATCTTTGATGTGAGAGACCAAAATGATCAGTGGATTCTGATAGCACTGAAGA	462
383	CGAGTCCGTACTTCCGATGTGAGGACAAAGGAGGACCAGTGGATCCGATCTTCATGCGAG	442
463	AAGGAGGACATGATTTCTGCCTCGAGGATCTACACCGCTTTTACGTTGAGCACCAGCA	522
443	AGGGAGACATGTCGACGCTCCCGCGGGATCTATCACCGCTTCACGGTGCAGCAGAGA	502
523	ACTATATCAAGCAATCCGACTGTTTGTGTGGCGATCTGTTTGGACACCCCTACACCGTC	582
503	ACTACAAGAGCCATCCGGCTGTTTGTGGGAGAACCGGTGTGGACACGCTACAAACGGC	562
583	CCCATGACCATCTTCCTCGCAAGAAAGAGTTTTTG	617
563	CCGCTGAGCATTTTGAAGCCCGCGGCATGACGTG	597

RESULT 12

US-09-840-787-77
; Sequence 77, Application US/09840787
; Patent No. US20020058264A1

GENERAL INFORMATION:
APPLICANT: Lal, Preeti
Hillman, Jennifer L.
Bandman, Olga
Shah, Purvi
Au-Young, Janice
Yue, Henry
Guegler, Karl J.
Corley, Neil C.

COLLEY, NEIL C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:

CONNECTED ADDRESS:
ADDRESS: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA

COUNTRY: USA
ZTP: 94304

```
,
, ZIE..IN300
, COMPUTER READABLE FORM:
, MEDIUM TYPE: Diskette
, COMPUTER: IBM Compatible
, OPERATING SYSTEM: DOS
, SOFTWARE: Fastseq for Windows version 2.0
, CURRENT APPLICATION DATA:
, APPLICATION NUMBER: US/09/840.787
,
```

FILING DATE: 23-APR-2001

? FILING DATE: 25 Apr 2001
 ? CLASSIFICATION: <unknown>
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 09/518,865
 ? FILING DATE: <unknown>
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: Billings, Lucy J.
 ?
 ?
 ?

```

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 77:
SEQUENCE CHARACTERISTICS:
LENGTH: 1107 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: LMODNOT03
CLONE: 1577239
SEQUENCE DESCRIPTION: SEQ ID NO: 77 :
US-09-840-787-77

```

Query Match 22.9%; Score 199.8; DB 10; Length 1107;
Best Local Similarity 61.7%; Pred. No. 3.5e-50;
Matches 318; Conservative 0; Mismatches 197; Indels 0; Gaps 0;

[illegible]

RESULT 13

```

US-09-878-574-3886
; Sequence 3886, Application US/09878574
; Patent No. US200201110548A1
; GENERAL INFORMATION:
; APPLICANT: Byrum, Joseph R.
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Thompson, Michael D.
; TITLE OF INVENTION: Nucleic Acid Molecules and
; TITLE OF INVENTION: plants
; FILE REFERENCE: 38-21(15401)B
; CURRENT APPLICATION NUMBER: US/09/878,574
; CURRENT FILING DATE: 2001-12-21
; PRIOR APPLICATION NUMBER: 09/733,535

```

	Query Match	20.9%	Score 182.4	DB 10	Length 706
	Best Local Similarity	60.4%	Prod. No. 4.7e-45		
	Matches 319	Conservative	0	Mismatches 206	Indels 3
	Gaps	1			
QY	93	AAAGCGAGGTGATAGAACATGTGTACATGGAT	---	GATAGCGAAGAGAGACGAGAGGCTT	149
DB	33	AAAGTCAGTGTGTTTTCGAGGCATGTTACATGAT	GAAGAGTCCGCGAGAGACCGACAGACTC	92	
YV	150	CCTCATACCGCGAACCACCAAGAAATTCATCTCTGTTGAT	AAAGCTTTACAGAACTTAGAGATA	209	

[illegible]

```

381 GAAATACGCTATTGTCTGAAGGAGTGGATCTTTGATGTGAGAGACCAAAATGATCAG 440
    || || ||||| || || || ||||| ||||| ||||| ||| | |||||
304 GAGATCCGCTACATCTGGATGGCAGTGGGTACTTCGATGTGAGGGACAAGGAGGACCGAG 363
    ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
441 TGGATTCGTATAGCACTCAAGAAAGGAGGCATGATGTTCTGCTCGCCTGCAGGGATGTACCAC 500
    ||||| || || ||||| ||||| ||||| ||||| ||||| ||||| |||||
364 TGGATCCGGATCTTCATGGAGAGGGAGACATGGTGACGCTCCCGCGGGGATCTATCAC 423
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
501 CGCTTTACGTTGGACACCGACAATATATCAAGGCAATGCGACTGTTTGTGGCGATCCT 560
    ||||| || ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
424 CGCTTCACCGTGGACGAGGAAGAACTACACGAAGGCCATGCGGCTGTTTGTGGGAGAACCG 483
    || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
561 GTTTGGACACCGCTACAACCGTCCCGATGACCATCTTCTGCAAGAAAGGAGTTTTGG 617
    || ||||| || ||||| ||||| ||||| ||||| ||||| ||||| |||||
    484 GTGTGGACAGCTACAACCGCGCCCGCTGACCATTTTGAAGCCCGCGGGGAGTACCTG 540
    )

```

Search completed: December 1, 2002, 22:49:06
 Job time : 112 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: December 1, 2002, 20:00:28 ; Search time 2187 Seconds

(without alignments)
6457,460 Million cell updates/sec

Title: US-09-785-738a-1

Perfect score: 872
Sequence: 1 agacgaacacacacagaat.....acagagatcatgaagctgaa 872

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database:

- 1: em_estba:*
- 2: em_esthm:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_hic:*
- 9: gb_estl:*
- 10: gb_estl2:*
- 11: gb_hic:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: gb_gss:*
- 18: em_gss_hum:*
- 19: em_gss_inv:*
- 20: em_gss_pin:*
- 21: em_gss_vtl:*
- 22: em_gss_fun:*
- 23: em_gss_mam:*
- 24: em_gss_mus:*
- 25: em_gss_other:*
- 26: em_gss_pro:*
- 27: em_gss_rtd:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	533.2	61.1	608	9	AU100980 AU100980
2	456.4	52.3	618	13	BM324741 PIC1_35_A
3	439.4	50.4	591	13	BM324752 PIC1_35_B
4	438	50.2	546	10	AM284744 LG1_214_H
5	421.6	48.3	700	9	AL504809 AL504809
6	419.8	48.1	1097	11	AY103746 AY103746

7	419.6	48.1	467	14	C28663	C28663	C28663 Rice
8	419.4	48.1	729	14	BO806508	BO806508	BO806508 WHE3579_H
9	418	47.9	574	10	AM678360	WS1_15_C1	AM678360 WS1_15_C1
10	417.8	47.9	600	13	BI542476		BI542476 949020B04
11	417.8	47.9	978	12	BG343468	HVSM8000	BG343468 HVSM8000
12	417.2	47.8	642	10	AV932455		AV932455 AV932455
13	417.2	47.8	642	13	BJ471108		BJ471108 BJ471108
14	417.2	47.8	644	14	BQ464906	HU02B15t	BQ464906 HU02B15t
15	417.2	47.8	709	13	BM370358	EBRC08_SQ	BM370358 EBRC08_SQ
16	417.2	47.8	840	12	BF6292917	HVSM8001	BF6292917 HVSM8001
17	417.2	47.8	890	14	BM816671	HC114G05_	BM816671 HC114G05_
18	416.6	47.8	605	14	BM244802	TAE15035C	BM244802 TAE15035C
19	416	47.7	715	14	BO805282	WHE3565_A	BO805282 WHE3565_A
20	415.6	47.7	697	14	BO755512	EBRC07_SQ	BO755512 EBRC07_SQ
21	415.6	47.7	794	12	BG299990	HVSM8002	BG299990 HVSM8002
22	414	47.5	563	10	AM126415	AM126415	AM126415 614071A04
23	414	47.5	693	10	BE215135	HV_CED000	BE215135 HV_CED000
24	412.4	47.3	793	12	BG367078	HVSM1001	BG367078 HVSM1001
25	411.2	47.2	611	14	BO466283	HT02B17r	BO466283 HT02B17r
26	410.8	47.1	802	10	BE195423		BE195423 HVSM8008
27	402.8	46.2	662	9	AL508895		AL508895 AL508895
28	401.4	46.0	560	9	AI947785	603028D09	AI947785 603028D09
29	399.6	45.8	583	14	BO758819	EBRC07_SQ	BO758819 EBRC07_SQ
30	397.8	45.6	566	10	AV915690	AV915690	AV915690 AV915690
31	396.8	45.5	589	10	AV941388	AV941388	AV941388 AV941388
32	396.8	45.5	626	10	AV922964	AV922964	AV922964 AV922964
33	396.6	45.5	549	14	BO249643	TAE25015G	BO249643 TAE25015G
34	393.4	45.1	548	14	BO238245	TAE05006E	BO238245 TAE05006E
35	393.2	45.1	713	12	BG463642	EM1_50_B1	BG463642 EM1_50_B1
36	390.8	44.8	584	9	AJ432173	AJ432173	AJ432173 AJ432173
37	390.2	44.7	613	14	BO238274	TAE05006B	BO238274 TAE05006B
38	389.8	44.7	585	14	BO458741	HA04F17r	BO458741 HA04F17r
39	389.4	44.7	871	13	BI951424	HVSM1002	BI951424 HVSM1002
40	389.2	44.6	608	14	BO238805	TAE05040H	BO238805 TAE05040H
41	387.6	44.4	464	14	C27474	Rice	C27474 Rice
42	387	44.4	524	14	BE403815	WHE0420_A	BE403815 WHE0420_A
43	384.4	44.1	493	14	BO282977	WHE3084_C	BO282977 WHE3084_C
44	381.8	43.8	562	14	BO758441	EBRC05_SQ	BO758441 EBRC05_SQ
45	381	43.7	575	10	AV939451		AV939451 AV939451

ALIGNMENTS

RESULT 1
AU100980
LOCUS
DEFINITION
AU100980 Rice callus Oryza sativa (japonica cultivar-group) cDNA
clone C61979, mRNA sequence.
ACCESSION
AU100980
VERSION
AU100980.1 GI:9865230
KEYWORDS
EST.
ORGANISM
Oryza sativa (japonica cultivar-group).
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzaceae; Oryza.
1 (bases 1 to 608)
REFERENCE
Sasaki, T. and Yamamoto, K.
Rice cDNA from callus (2000)
Unpublished (2000)
JOURNAL
Contact: Yakuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
Email: tsasakie@affrc.go.jp, URL: http://rgp.dna.affrc.go.jp/
PROJECT = "RGP".
FEATURES
source
location/Qualifiers
1..608
/organism="Oryza sativa (japonica cultivar-group)"
/cultivar="Nipponbare"

```

/db_xref="taxon:39947"
/clone_lib="Rice callus"
/note="Vector: pBluescript II SK+; Site.1: SalI; Site.2:
NotI; cDNA prepared from rice callus mRNAs by using
oligo(dT) as a primer and ligating to the SalI-NotI site
of pBluescript II SK+ phagemid."
BASE COUNT      198 a      111 c      131 g      166 t      2 others
ORIGIN
Query Match      61.1%; Score 533.2; DB 9; Length 608;
Best Local Similarity 97.3%; Pred. No. 8,8e-155;
Matches 541; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 310 GCCCAGAGAAAGTGGCCAAATTATGAACATAAGATCTTCTTGAGACACCTGC 369
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 6 GCCCANAGAAAGCTGCCAAATTATGAACATAAGATCTTCTTGAGACACCTGC 65
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 370 ATACCGATGAAGAAATACGCTATGTCTGAGGAGGAGTCTTCTGAGAGACC 429
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 66 ATACCGATGAAGAAATACGCTATGTCTGAGGAGGAGTCTTCTGAGAGACC 125
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 430 AAAATGATCAGTGGATTCTGTATGACATGAGAAAGAGGAGCATGTCTGCTGCAG 489
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 126 AAAATGATCAGTGGATTCTGTATGACATGAGAAAGAGGAGCATGTCTGCTGCAG 185
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 490 GGATGTACCAACCGCTTACCTGAGACGACATCTATTCAGGCATGCGACTGTTTG 549
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 186 GGATGTACCAACCGCTTACCTGAGACGACATCTATTCAGGCATGCGACTGTTTG 245
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 550 TTGGGATCTGTTTGGACACCTTACACCCGTCGCCATGACCATCTTCTGCAAGAAAG 609
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 246 TTGGGATCTGTTTGGACACCTTACACCCGTCGCCATGACCATCTTCTGCAAGAAAG 305
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 610 AGTTTGGCTAAACTTCACAGTCAAGAGGAGGAAATTCAGCATTTAGAGCTTTGAG 669
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 306 AGTTTGGCTAAACTTCACAGTCAAGAGGAGGAAATTCAGCATTTAGAGCTTTGAG 365
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 670 GGTTTTGTGGCTCTGACACTGCGGTCTATATTCACAGTGAATAGATGCTATAGC 729
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 366 GGTTTTGTGGCTCTGACACTGCGGTCTATATTCACAGTGAATAGATGCTATAGC 425
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 730 AATGTAATTTAGCACAGAGGCTGATGCGCCATCACCACCTTAAAGTGAAGATTAA 789
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 426 AATGTAATTTAGCACAGAGGCTGATGCGCCATCACCACCTTAAAGTGAAGATTAA 485
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 790 TGATTTTGTGAATCTTATGATCAATCGCATATAGCATTTCCGAATGTGTTTCAA 849
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 486 TGATTTTGTGAATCTTATGATCAATCGCATATAGCATTTCCGAATGTGTTTCAA 545
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 850 TAAACAGAGTCAATGA 865
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 546 TAAACAGAGTCAATGA 561
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 2
BM324741
LOCUS      BM324741
DEFINITION PIC1.35.A12.b1.A002 pathogen-infected compatible 1 (PIC1) Sorghum
            bicolor cDNA, mRNA sequence.
ACCESSION  BM324741
VERSION    BM324741.1
KEYWORDS   EST.
SOURCE     sorghum.
ORGANISM   Sorghum bicolor
            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
            clade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE  1 (bases 1 to 618)
            Cordonnier-Pratt,M.-M., Gingle,A., Fang,G.C., Dean,R., Wing,R.,
            Sudman,M. and Pratt,L.H.
            An EST database from Sorghum: plants infected with a compatible
            pathogen
TITLE

```

JOURNAL COMMENT

Unpublished (2002)
 Contact: Cordonnier-Pratt MM
 Laboratory for Genomics and Bioinformatics
 The University of Georgia, Department of Plant Biology
 Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
 Tel: 706 542 1860
 Fax: 706 583 0210
 Email: mmp@pratt.uga.edu
 Sequences have been trimmed to exclude PolyA, vector, and regions
 below Phred quality 16. The threshold for highest quality sequence
 is 20. Three-prime sequences, which are obtained with PolyMix or
 T7 sequencing primer, are presented as the reverse complement.
 Seq primer: JEN REV
 High quality sequence stop: 604
 POLYA-No.

FEATURES

```

source      location/qualifiers
1..618
/organism="Sorghum bicolor"
/cultivar="Brx623"
/db_xref="taxon:4558"
/clone_lib="Pathogen-infected compatible 1 (PIC1)"
/lssue_type="Leaves"
/dev_stage="4-week-old seedlings infected with
Colletotrichum graminicola"
/note="Vector: pBluescript II SK(-) from Lambda zap II;
Site.1: XhoI; Site.2: EcoRI; Four-week-old sorghum
seedlings were sprayed with spore suspension prepared from
3-week-old FRM421, a sorghum isolate of the anthracnose
pathogen Colletotrichum graminicola. Inoculated plants
were kept in a 25 C dark growth chamber with 100% relative
humidity for 24 hr, followed by 12/12 hr of light/dark
cycle at 25 C with 90% relative humidity for another 24
hr. All leaves were harvested and quick frozen with liquid
nitrogen and stored in a -80 C freezer. The library was
made from poly-A RNA in the cloning vector lambda Zap II.
Clones to be sequenced were prepared by mass excision.
WARNING: While most or all ESTs are expected to derive
from the host plant, no effort was made to eliminate ESTs
deriving from the pathogen."
BASE COUNT      187 a      124 c      162 g      145 t
ORIGIN
Query Match      52.3%; Score 456.4; DB 13; Length 618;
Best Local Similarity 89.0%; Pred. No. 7.9e-131;
Matches 493; Conservative 0; Mismatches 61; Indels 0; Gaps 0;

```

```

QY 65 CCACATGGAGAAACCAATTCAGATGTAAGACGAGTGAAGACATGGTACATGA 124
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 63 CACACATGGAAACCCAGATGCCAGATGTAAGACGAGATTTAGAACATGGTACATGA 122
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 125 TGATAGCGAAGAGACAGAGGCTTCTGATCAACGCCGCAACCCAAAGAAATTCCTCTG 184
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 123 CGATAGTGAAGAAAGACAGAGGCTTCTGATCAACGCCGCAACCCAAAGAAATTCCTCTG 182
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 185 TGATAGGCTTACAGACAGAGATTAATCAGCTGGCGCTAAATCCGTGAATCTGGAGAA 244
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 183 TGATAGGCTTACAGACAGATTAATCAGCTGGCGCTAAATCCGTGAATCTGGAGAA 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 245 TTGCGAGAACCTGGAAGAAATCCGCGAAGAGGATTAATGTTGACATTTGTA 304
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 243 TGATGAGAACTCAAGAAATCCGCGAAGAGGATTAATGTTGACATTTGTA 302
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 305 TGTGTGCCAGAGAAAGCTGCCAAATTAATGAATGATCAAGATTTCTTGAAGACA 364
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 303 TGTATGCCAGAGAAAGCTGCCAAATTAATGAATGATCAAGATTTCTTGAAGACA 362
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 365 CCGTCAATACCGATGAAGAAATAGCGTAATGCTTGAAGAGAGTGAATCTTGAATGATGAG 424
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 363 CCGTCAATACCGATGAAGAAATAGCGTAATGCTTGAAGAGAGTGAATCTTGAATGATGAG 422
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 425 AGACCAAAATGATGAGTGGATTTGATAGACGAGAAAGAGACATGATTTGTTGCC 484
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 423 GACGCAAAATGATGAGTGGATTTGATAGACGAGAAAGAGACATGATTTGTTGCC 482
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

FEATURES	source
RESULT 3	
LOCUS	BM324752
DEFINITION	BM324752 591 bp mRNA linear EST 04-JAN-2002
ACCESSION	PICT1_35.B12.B1_A002 Pathogen-infected compatible 1 (PICT1) Sorghum
VERSION	BM324752
KEYWORDS	BM324752.1 GI:18063663
SOURCE	EST.
ORGANISM	sorghum.
REFERENCE	Sorghum bicolor
AUTHORS	Eukaryota: Viridiplantae; Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales; Poaceae; PACC
TITLE	Clade: Panicoideae; Andropogoneae; Sorghum.
JOURNAL	1 (bases 1 to 591)
COMMENT	Cordonnier-Pratt,M.-M., Gingle,A., Fang,G.C., Dean,R., Wing,R., Sudman,M. and Pratt,L.H.
	An EST database from Sorghum: plants infected with a compatible pathogen
	Unpublished (2002)
	Contact: Cordonnier-Pratt MM
	Laboratory for Genomics and Bioinformatics
	The University of Georgia, Department of Plant Biology
	Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
	Tel: 706 542 1860
	Fax: 706 563 0210
	Email: mmpatt@uga.edu
	Sequences have been trimmed to exclude PolyA, vector, and regions below Phred quality 16. The threshold for highest quality sequence is 20. Three-prime sequences, which are obtained with PolyTmix or 17 sequencing primer, are presented as the reverse complement.
	Seq primer: JEN REV
	High quality sequence stop: 442
	PolyA=NO.
	Location/Qualifiers
	1..591
	/organism="Sorghum bicolor"
	/cultivar="Brix623"
	/db_xref="taxon:4558"
	/clone_lib="Pathogen-infected compatible 1 (PICT1)"
	/tissue_type="Leaves"
	/dev_stage="4-week-old seedlings infected with
	Colletotrichum graminicola"
	/note="Vector: pBluescript II SK(-) from Lambda Zap II;
	Site_1: XhoI; Site_2: EcoRI; Four-week-old sorghum
	seedlings were sprayed with spore suspension prepared from
	3-week-old FRM421, a sorghum isolate of the anthracnose
	pathogen Colletotrichum graminicola. Inoculated plants
	were kept in a 25 C dark growth chamber with 100% relative
	humidity for 24 hr, followed by 12/12 hr of light/dark
	cycle at 25 C with 90% relative humidity for another 24
	hr. All leaves were harvested and quick frozen with liquid
	nitrogen and stored in a -80 C freezer. The library was
	made from poly-A RNA in the cloning vector lambda Zap II.
	Clones to be sequenced were prepared by mass excision.
	WARNING: While most or all ESTs are expected to derive
	from the host plant, no effort was made to eliminate ESTs
	deriving from the pathogen."

Query Match	50.4%	Score 439.4	DB 13	Length 591
Best Local Similarity	89.4%	Pred. No.1,5e-125		
Matches 473	Conservative 0	Mismatches 56	Indels 0	Gaps 0
QY 65	CCACATGAGAAACGAATTCACAGATGGTATGACACGAGATATATGAAAGCATGGTACATGGA	124		
Db 63	CAACATGGAACCGAGTTCACAGATGGTAAACACAGAGATTAATGAAAGCATGGTACATGGA	122		
QY 125	TGATAGCGAAGAGGACCCAGAGCTTCCTCCATCACACCGCGGAACCCCAAGAAATTCATCTCT	184		
Db 123	CGATATCTGAAGAAGACACAGAGCTTCCTCCATCACACCGCGATCCCAAGAAATTCATCTCT	182		
QY 185	TGATATGCTTACAGAACTGATATACGTGGCGCTTAATCTCGATTAACGGGGAGAA	244		
Db 183	TGATATGCTTACAGACTGATATACGTGGCGCTTAATCTCGATTAACGGGGAGAA	242		
QY 245	TTTCGAGAACCTGAAAGAGAAATCCGCGAAGCCAGAGTTACTTTATGTGGACATTTTGGA	304		
Db 243	TGATGAGAACCTCAAGAAATCCGCGAAGCCAGAGTTACTTTATGATGACATTTTGGA	302		
QY 305	TGATGCCCCAGAGAGCTGCCAAATTTATGAACATACATCCAGGTTCTTTTAAAGACA	364		
Db 303	TGATATCCCCAGAGAGCTGCCAAATTTATGAATTAAGTAAAGAAATTTCTTTTAAAGACA	362		
QY 365	CTGTCATACCGATGGAAGAATACGTTATGTTCTTGAAGGAGTGGATCTTTGATGTGAG	424		
Db 363	CTGTCATACCGATGGAAGAATACGTTATGTTCTTGAAGGAGTGGATCTTTGATGTGAG	422		
QY 425	AGACCAAAATGATTCAGATGATTCGATATGACACTGAAGAAAGAGGCACTGATTTGTGGC	484		
Db 423	GGACGAAATGACACGATGATTCGATATGACACTGAAGAAAGAGGCACTGATTTGTGGC	482		
QY 485	TGCAGGATGATACCAACCGCTTACGTTGAGACACCGACACACTATATTCAGGCAATGCGCAT	544		
Db 483	TGCAGGATGATACCAACCGCTTACATTTGACAAATATATATATATATATATATATATATAT	542		
QY 545	GTTTGTGGGATCTGTTTGGACACCGCTTACACCGCTCCCATGACCAT	593		
Db 543	CTTGTGGGAGCCGTGTTGGACCGCTTACACCGCTCCCATGATCAT	591		
RESULT 4				
LOCUS	AW284744/c	546 bp	mrna	linear
DEFINITION	LG1_214.H12.g1_A002 Light Grown 1 (LG1) Sorghum bicolor CDNA, mRNA			
ACCESSION	AW284744			
VERSION	AW284744.1			
KEYWORDS	EST			
SOURCE	Sorghum			
ORGANISM	Sorghum bicolor			
REFERENCE	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Sorghum.			
AUTHORS	1 (bases 1 to 546)			
JOURNAL	Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C. and Pratt,L.H.			
COMMENT	An EST database from Sorghum: light-grown seedlings unpublished (2000)			
Contact: Cordonnier-Pratt MM				
Laboratory for Genomics and Bioinformatics				
The University of Georgia, Department of Plant Biology				
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA				
Tel: 706 542 1860				
Fax: 706 583 0210				
Email: mmp@pratt.uga.edu				
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.				
Seq. primer: #7				
High quality sequence start: 7				
High quality sequence stop: 546				
PolyA-No.				

Seq primer: T3 primer for 5' end.

1. .700

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/organism="Hordeum vulgare"
/cultivar="Barke"
/db_xref="taxon:4513"
/clone="HW06H13v"
/clone_1lb="Hordeum vulgare Barke roots"
/tissue_type="roots"
/lab_host="XLDR"

```

XhoI; mRNA was made from roots of spring barley variety

for two days on filter paper at room temperature Cloning

NOTE: Due to a cloning artefact caused by the kit, in most

adapter. Average insert size is 1 kb Sequence trimming:

ambiguities. The maximum length was set to 700 bp.

STAINING 4 120 5 654 6 607

48.38; Score 421.6; DB 9; Length 700;

199; Conservative 0; Mismatches 130; Indels 0; Gaps 0

AAAGTTCCGCTCTTGCTTCCACCCCGCAATCCACATGGAGAACGAATTCACGATGGTAA 94

CAGTTGCGCGGAGACTGCGAGGGGCCCGCCATGGAGAACGAGTTCACGATGGCA 91

ACGGAGGTCATAGAAAGCATGGTACATGGATAGCGAAGAGGACCAGAGGCTTCCTCA 154

3AGCAGGTCATCCAAACATGGTACATGGATGACAGTGAAGAGGACCCAGAGGCTTCCTCA 151

CAACCGGAACTCATTCCGGTGAATAGCTTACAGAACCTTAGGAGTAATCAG 214

[illegible]

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TTGAGGGCAGTGGATCTTGCATGTGAGGGACCAAAACGAACAGTGGATCCGATAGC 451

CTGAAGAAGGAGGCATGATTGTTCTGCGCTGCAGGATGTACCACCGCTTTACGTTGGA 514

5TTAAGAAGCGGCATGTTGTTTGCCCTGCAGGAATGTATCACCGCTTACATTGA 511

ACCGACACTATATCAAGGCAATGGACTGTTGTTGGCGATCCTGTTGGACACCCTA 574

AGTGACAACTACATCAAGGCAATGCGCTCTTTGTGGAGAGCCCATCTGGACGCCGTA 571

AAACCGTCCCGCATGACCATCTTCCCTGCAAGAAAGGAGTTTGGCTAAACTTCTCAAGTC 634

AAATCGCCCCCATGACCATCTCCAGCTAGAAAGGAGTTATTGTCGACAGATTATCAAC 631

5AAGGTGAAATCAAGCAGTTGAAGGCT 663

5'GATGTTGGAGCCCAACCCGTTTCGAGGCT 660

[illegible][illegible]

QY	488	AGGATGTACCCACCGTTTACGTTGGACACCGACAACTATATCAAGGCATGCACTGTT	547
Db	624	AGGAATGTATCATCGCTTTACGTTGGATGATGACACACTCATCAAGGCATGCGTCTATT	683
QY	548	TGTTGGGATCATCTGTTTGGACACCCCTACACACCGTCCCATGACCATCTCTGTGCAGAAA	607
Db	684	TGTGGGTGAGCCCTGCTGTGACACACATACATCTGTCGCATGACCATCTCCCGGCTAGSAA	743
QY	608	GGAATTTTTGGCTAAACCTTCTCAATCTCAAGAGGTGAAAATTCAAAGCATTTGAAGGCTTCTG	667
Db	744	GGAATTAAGCTTCGAAATAATCATCA---CCGAGGTGGAAGAACCGATCGAAAGCTGGTTG	800
QY	668	AGGGTTT	674
Db	801	AGCGTCT	807

RESULT 7	
C28663 LOCUS	467 bp mRNA linear EST 04-APR-2002
DEFINITION	C28663 Rice callus cDNA Oryza sativa (japonica cultivar-group) cDNA clone C61979_1A, mRNA sequence.
ACCESSION	C28663
VERSION	C28663.1 GI:2312508
KEYWORDS	EST.
SOURCE	Oryza sativa (japonica cultivar-group).
ORGANISM	Oryza sativa (japonica cultivar-group); Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartioideae; Oryzaceae; Oryza.
REFERENCE	Yamamoto, K. and Sasaki, T. Rice cDNA from callus 1997 Unpublished (1997)
AUTHORS	Contact: Takuji Sasaki
TITLE	National Institute of Agrobiological Resources
JOURNAL	Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki 305-8602, Japan
COMMENT	Tel: 81-298-38-7441 Fax: 81-298-38-7468 Email: tsasak@abdr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/ PROJECT = "RGP".
FEATURES	Location/Qualifiers
SOURCE	1..467
	/organism="Oryza sativa (japonica cultivar-group)"
	/cultivar="Nipponbare"
	/db_xref="taxon:39947"
	/clone="C61979_1A"
	/clone_1lb="Rice callus cDNA"
	/tissue_type="callus"
	/dev_stage="callus"
	/note="Organ: panicle; Rice cDNA from panicle at ripening stage"
BASE COUNT	150 a 92 c 119 g 104 t 2 others
ORIGIN	
Query Match	48.1%; Score 419.6; DB 14; Length 467;
Best Local Similarity	97.2%; Pred. No. 2,1e-119;
Matches 447; Conservative	0; Mismatches 11; Indels 2; Gaps 2;
OY	1 AGAGCAACAANAACGATTCATCGCCCATATGGAAGTTCGCTCTTGCTCCACC CGG 60
DB	8 AGAGCAACAANAACGATTCATCGCCCATATGGAAGTTCGCTCTTGCTCCACC CGG 67
OY	61 CAATCCACATGAGAGCAATTCCAGAGATGGTAAGAAGCAGAGATGATGAAGCATGTGTACA 120
DB	68 CAATCCACATGAGAGCAATTCCAGAGATGGTAAGAAGCAGAGATGATGAAGCATGTGTACA 127
OY	121 TGG-ATATATGCCAAAGAACCGAGAGCTTCTCTATCACCGCGGAACCCAAAGATTCATT 179
DB	128 TGGAATGATAGCAAGAAGACGAGAGGCTTCTCTATCACCGCGGAACCCAAAGATTCATT 187

QY 180 CCTGTTGATGACTTACAGACTAGAGTAAATCAGCTGGCCCTAAATCTGATACTG 239
 Db 188 CATGTTGATGACTTACAGACTAGAGTAAATCAGCTGGCCCTAAATCTGATACTG 247
 QY 240 GAGATTCCGAGAACTGGAAGAAATCCGCGAAGCCAGAGTACTTATGT-GGACAT 288
 Db 248 GAGATTCCGAGAACTGGAAGAAATCCGCGAAGCCAGAGTACTTATGTGGGACAT 307
 QY 299 TTGTTGATGTTGGCCAGAGAGTGGCCAAATATGAACTAGATCAAGATTTCTTGA 358
 Db 308 TTGTTGATGTTGGCCAGAGAGTGGCCAAATATGAACTAGATCAAGATTTCTTGA 367
 QY 359 AGAACACCTGCATACCGATAGAGAAATAGCATTTGCTTGAAGGAGTGCATCTTGA 418
 Db 368 AGAACACCTGCATACCGATAGAGAAATAGCATTTGCTTGAAGGAGTGCATCTTGA 427
 QY 419 TGTGAGAGACCAAAATGATCATGTGATCTATAGACATG 458
 Db 428 TGTGAGAGACCAAAATGATCATGTGATCTATAGACATG 467
 RESULT 8
 LOCUS B0806508 729 bp mRNA linear EST 31-JUL-2002
 DEFINITION WHE3579_H05_0092S wheat developing grains cDNA library Trilicium
 accession B0806508
 VERSION B0806508
 KEYWORDS B0806508.1 GI:22030717
 SOURCE EST.
 ORGANISM bread wheat.
 Trilicium aestivum
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poaceae;
 1 (bases 1 to 729)
 Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin,
 K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Raue, C.J.,
 Wilson, C., and Woo, J.
 The structure and function of the expressed portion of the wheat
 genomes - Developing grains cDNA library
 Contact: Olin Anderson
 US Department of Agriculture, Agriculture Research Service, Pacific
 West Area, Western Regional Research Center
 800 Buchanan Street, Albany, CA 94710, USA
 Tel: 5105595773
 Fax: 5105595818
 Email: oanderson@w.usda.gov
 Sequences have been trimmed to remove vector sequence and low
 quality sequence with phred score less than 20
 Seq primer: SK primer.
 FEATURES
 SOURCE
 location/Qualifiers
 1..729
 /organism="Trilicium aestivum"
 /cultivar="Butte 86"
 /db_xref="taxon:4565"
 /clone_lib="WHE3579_H05_009"
 /issue_type="whole grains"
 /dev_stage="3-44 days post anthesis seed"
 /lab_host="E. coli SOLR"
 /note="Vector: Lambda ZAP II, excised phagemid; Site 1:
 EcoRI; Plants were grown under six following different
 environmental regimes in greenhouse, Environment 1)
 240C/170C day/night, well-watered, with post-anthesis
 fertilizer, Environment 2) 240C/170C day/night,
 well-watered, without post-anthesis fertilizer,
 Environment 3) 370C/170C day/night, well-watered, with
 post-anthesis fertilizer, Environment 4) 370C/170C
 day/night, well-watered, without post-anthesis fertilizer,
 Environment 5) 370C/170C day/night plus drought, with
 post-anthesis fertilizer, Environment 6) 370C/170C
 day/night plus drought, without post-anthesis fertilizer,

developing wheat grains from the following were excised
 and frozen in liquid nitrogen, Environment 1 at 3, 5, 7,
 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44 DPA Environment
 2 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28, 32, 36, 40, 44
 DPA Environment 3 at 3, 5, 7, 8, 10, 12, 16, 20, 24, 28,
 32, 34 DPA Environment 4 at 3, 5, 7, 8, 10, 12, 16, 20, 24,
 28, 32, 34 DPA Environment 5 at 3, 5, 7, 8, 10, 12, 16,
 20, 24, 28, 30 DPA Environment 6 at 3, 5, 7, 8, 10, 12, 16,
 20, 24, 28, 30 DPA and total RNA was prepared by S.
 Altenbach and K. Cronin at USDA-ARS, Albany, CA. A cDNA
 library was made using poly (A) RNA, and the cDNA clones
 were in vivo excised to give phagescript SK(-) phagemids
 in the TJ Close lab (Chin, Close, Fenton) at the
 University of California, Riverside. Plasmid DNA
 preparations and DNA sequencing were performed in the OD
 Anderson lab (others).
 BASE COUNT 213 a 151 c 206 g 159 t
 ORIGIN
 Query Match 48.1%; Score 419.4; DB 14; Length 729;
 Best Local Similarity 78.7%; Freq. No. 2,9e-119;
 Matches 514; Conservative 0; Mismatches 136; Indels 3; Gaps 1;
 QY 42 CGCTCTTGCTTCACCCCGCATCCATGAGAGCAATTCGAGATGTAAGACGGAG 101
 Db 35 CGCTTGAGACTGCAGAGAGCCCGCCCATGAGAGAGTCCAGGATGCAAGAGGAG 94
 QY 102 GTGATAGAGCAATGTATCATGATGATGATGATGATGATGATGATGATGATG 161
 Db 95 GTATCCAGCATGTATCATGATGATGATGATGATGATGATGATGATGATGATG 154
 QY 162 GAACCCAAAGATTCATCTCTGTTGATGATGATGATGATGATGATGATGATG 221
 Db 155 GACCCCAAGAGTTCATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 214
 QY 222 CTAAATCTGATTAACCTGAGAGAGATGATGATGATGATGATGATGATGATGAT 281
 Db 215 CTGATGCTGATTAACCTGAGAGAGATGATGATGATGATGATGATGATGATGAT 274
 QY 282 TACTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 341
 Db 275 TACTCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 334
 QY 342 ATCAAGATTTCTTGAAGAGAGATGATGATGATGATGATGATGATGATGATG 401
 Db 335 CTGAAGATTTCTTGAAGAGAGATGATGATGATGATGATGATGATGATGATG 394
 QY 402 GGGAGTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 461
 Db 395 GCGAGTGAATCTGATGATGATGATGATGATGATGATGATGATGATGATGATG 454
 QY 462 AAGAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 521
 Db 455 AAGAGAGCATGATGATGATGATGATGATGATGATGATGATGATGATGATG 514
 QY 522 AACTATATCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 581
 Db 515 AACTATATCAAGAGAGATGATGATGATGATGATGATGATGATGATGATGATG 574
 QY 582 CCCATGACCATCTCTCTGCAAGAAAGAGTTTGGCTTAACCTTCAAGTCAAG 641
 Db 575 CCCATGACCATCTCTCTGCAAGAAAGAGTTTGGCTTAACCTTCAAGTCAAG 631
 QY 642 GAAATATCAAGAGAGAGTCTGAGAGGTTTGGCTTCAAGTCAAGTCAAGTCA 694
 Db 632 GGAATCAAGAGAGAGTCTGAGAGGTTTGGCTTCAAGTCAAGTCAAGTCAAG 684
 RESULT 9
 LOCUS AW678360 574 bp mRNA linear EST 19-JUL-2000
 DEFINITION WS1_15_C10_b1-A002 water-stressed 1 (WS1) Sorghum bicolor cDNA,
 mRNA sequence.

Accession	Version	KeyWords	Source	Organism
AM678360	1	GI:7552089	Sorghum bicolor	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC lade; Panicoideae; Andropogoneae; Sorghum.
REFERENCE AUTHORS				L.H., Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt ,L.H.
TITLE				An EST database from Sorghum: water-stressed plants
JOURNAL				Unpublished (2000)
COMMENT				Contact: Cordonnier-Pratt MM Laboratory for Genomics and Bioinformatics The University of Georgia, Department of Plant Biology Plant Sciences Building, Rm. 250Z, Athens, GA 30602-7271, USA Tel.: 706 342 1860 Fax: 706 583 0210 Email: mmp@prattuga.edu
FEATURES				Seq primer: JEN REV High quality sequence stop: 512 POLY-A-No.
source				Location/Qualifiers 1..574 /organism="Sorghum bicolor" /db_xref="taxon:4558" /clone_lib="Water-stressed 1 (WS1)" /note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."
BASE COUNT				166 a 126 c 144 g 138 t
ORIGIN				
Query Match				47.9%; Score 418; DB 10; Length 574;
Best Local Similarity				87.5%; Pred. No. 7.2e-119;
Matches 457:				Conservative 0; Mismatches 65; Indels 0; Gaps 0;
OY 135	GAGGACCGAAGGCTTCATCACCGCGCAACCAGAATTCACTTGGTTGAATAAGCTT			194
DB 9	GAAGACGAGAGCTCCCTCATCCCGTGATGCCAAGAAATTCATTCTCTGTGAATGCCTT			68
OY 195	ACGAACCTAGGACTAATGACGTCGCGCCCTAAATCTGTATATCGGGAATTCGCGAAC			254
DB 69	TCAAACTCGGATCATCAGCTBGCCTCGAATCTTGACAACTGGAGAAATGATGAGAAC			128
OY 235	CTGAGAGAAATCCGCGAAGCAGAGGTTACTCTTATGTGGACATTTTGATGTGGCCA			314
DB 129	CTCAAGAAATCCGTGAAGCAGAGGCTACTCTTCATGACATTTGTGATGTATGCCA			188
OY 315	GAGAAGCTGCCAAATTTATGAAACTAAGATCAAGAGATTTCTTTGAAGAACAACCTGCATACC			374
DB 189	GAGAAGCTGCCAAATTTATGAGATTAAGATTAAGAAATTTCTTTGAAGAACAACCTGCATACC			248
OY 375	GATGAAGAAATPACGCTAATGTGCTGGAAGGAGATGGATCTTGATGTGAGAACCCAAAT			434
DB 249	GATGAAGAAATPACGCTAATGTGCTTGGAAGGAGATGGATCTTGATGTGAGAGAGCAAAT			308
OY 435	GATAGTGGATGCTGATAGCACTGAAGAAGAGGACGATGATTTGTTGCCCTGCAGGATG			494
DB 309	GACCAAGTGATCGGTGTAGAGTGAAGAAAGAGACGATTTGTTCTTCGACAGGATG			368
OY 495	TACCAACGCTTTTACGTTGGACACCGCAACATTTATCAAGGCAATGCACATGTTTGTGGC			554
DB 369	TATCACCGCTTACATTTGGACATGACATGTAATCAAGGCAATGCGCTTTTGTGGC			428
OY 545	GATCCTGTTTGGACACCTTCAGACGCTCCGCAATGACATTTCTTCGAACAAGAGATTT			614

Db	429	GACCCTGTTTGACGCCGCTACAAACCGTCCCATGATCATCGCAGCAGCAAGAGTAT	488
Oy	615	TTGGCTAAACTTCTCAGTCAGACAGCTAATAANTCAACACTT	656
Db	489	CTGGACAAAGCTCTCTCAAGCCAGAAAGCCACAGCTTTGAGCT	530
RESULT 10			
BI542476		600 bp	linear
LOCUS		949020B04.Y1 949	- Juvenile leaf and shoot cDNA from Steve Moose
DEFINITION		Zea mays cDNA, mRNA sequence.	
ACCESSION		BI542476	
VERSION		BI542476.1	GI:15426554
KEYWORDS		EST.	
SOURCE		Zea mays.	
ORGANISM		Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophytes; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC	
REFERENCE		clade; Panicoideae; Andropogoneae; Zea.	
AUTHORS		1 (bases 1 to 600)	
TITLE		Maize ESTs from various cDNA libraries sequenced at Stanford University	
JOURNAL		Unpublished (1999)	
COMMENT		Contact: Walbot V Department of Biological Sciences Stanford University 855 California Ave, Palo Alto, CA 94304, USA Tel: 650 723 2227 Fax: 650 725 8221 Email: walbot@stanford.edu Plate: 949020 row: B column: 04. location/Qualifiers 1. 600 /organism="Zea mays" /cultivar="W66A" /db_xref="taxon:4577" /clone_lib="949 - Juvenile leaf and shoot cDNA from Steve Moose" /tissue_type="Immature leaf primordium and vegetative meristem" /dev_stage="4 stages from 3-13 days after imbibing" /lab_host="E. coli XL0LR" /note="Organ: juvenile vegetative shoots; Vector: pMD-GAL4-2.1; Site:1; EcoRI; Site:2; XhoI; Equal amounts of total RNA by weight from 4 tissue sources (see below) were pooled, polyA+ RNA isolated, and cDNA synthesized for EcoRI (5') and XhoI (3') directional cloning into lambda Hybridex vector from Stratagene. Tissue sources: 1. Whole shoots 3 days after sowing/imbibing in wet soil.; 2. Basal 1.5 cm shoots 6 days after sowing - Includes yellow portions of developing leaves 1-5, primordia from 6-8, and the vegetative apex. 3. Non-green portions of developing leaves 4-5 and the vegetative apex, including adult leaf primordia, 9 days after sowing. 4. Partially expanded and greening leaves 4-5 at 13 days after sowing."	
BASE COUNT		173 a 123 c 167 g 137 t	
ORIGIN			
Query Match		47.9%	Score 417.8; DB 13; Length 600;
Best Local Similarity		83.1%	Pred. No. 8.5e-119;
Matches 476; Conservative		0; Mismatches 97; Indels 0; Gaps 0;	
Oy	68	CATGAGAACGAATTCACAGATGATTAAGACGAGGTGATTAAGACCATGGTATCGATGA	127
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Oy	128	TAGGAAGACGACCAAGGCTTCATACCGCCAAACCCAAAGAATTCATTCCTGTTGA	187
Db	76	CATGGAAGAGACCAAGGCTTCATCATCTGTCGAGCCCAAAATAATTCCTCTCGCA	135
Oy	188	TAACTTACAGAACTAGAGACTAATCAGCTGGCGCCTTAATCTCTGATTAATCTGGGAGATTTG	247


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Db      136 CAAACTTCCGACTAGGATATTAACTGGGCGGCTTAATGCTGATGATTTGGGAGATGA 195
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QY      428 CCAAAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 487
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DEFINITION   HVSME90005N13f Hordeum vulgare pre-anthesis spike EST library
              HVCNDA0008 (white to yellow anther) Hordeum vulgare cDNA clone
              HVSME90005N13f, mRNA sequence.
ACCESSION   BG343468
VERSION     BG343468
KEYWORDS    EST.
SOURCE      Hordeum vulgare.
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            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
            Triticeae; Hordeum.
REFERENCE   1 (bases 1 to 978)
            Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu
            Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Choi, D.W., Fenton
            R.D., Close, S.J., Oates, R. and Main, D.
            Development of a genetically and physically anchored EST resource
            for barley genomics: Morex pre-anthesis spike cDNA library
            Unpublished (2001)
JOURNAL     Contact: Ming RA
COMMENT     Clemson University Genomics Institute
            100 Jordan Hall, Clemson, SC 29634, USA
            Tel: 864 656 7288
            Fax: 864 656 4293
            Email: twing@clemson.edu
            Total hg bases = 505
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/note="Vector: JambazAP, Site_1: EcoRI, Site_2: XhoI;
Plants were grown in the greenhouse at the University of
California, Riverside (Fenton, SJ Close, TJ Close). Whole
spike with awns trimmed were collected at white, green and
yellow anther stages (Fenton). Total RNA was prepared from
each pool, equal quantities of all three RNA pools were
combined, poly(A) RNA was purified from the mixture, one
primary unamplified cDNA library was made, and 1 million
pfu were in vivo excised to give phuscript SK(-) cDNA
phagemids. These steps were performed in the TJ Close lab
(Choi) at the University of California, Riverside.
Phagemids were plated and picked at the Clemson University
Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins
and Wing) Plasmid DNA preparations, DNA sequencing and
sequence analysis were performed at CUGI (Wing, Yu, Frisch
, Henry, Simmons, Oates, Rambo, Main). The sequence has
been trimmed to remove vector sequence and contains a
minimum of 100 bases of phred value 20 or above. For more
details on library preparation and sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ, Wing R, Kleinhofs A, Wise R (2001)
Genetically and Physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/g9pages/bgn/31/cover.html)"
BASE COUNT      275 a      275 g      219 t
ORIGIN
Query Match      47.9% Score 417.8; DB 12; Length 978;
Best local similarity 80.5%; Pred. No. 1e-118;
Matches 488; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
QY      35 GAAAGTTCCTCTCTCCACCCCGCATTCACATGACAGAACATTCAGATGTAA 94
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QY      215 CTGGCCCTTAATCTCTGATTAAGTGGAGAAATTCGAGAACCTGAGAGATCCGGAAC 274
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 Hordeum vulgare.
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae
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 1 Trilicene: Hordeum.
 Zhang, H., Potokina, E., Michalek, W., Weschke, W., Stein, N. and Graner
 A.
 TITLE Barley ESTs from germinating seeds
 JOURNAL Unpublished (2002)
 COMMENT Contact: Stein Nils
 Molecular Markers Group, Department Genbank
 Institute of Plant Genetics and Crop Plant Research (IPK)
 Corrensstr. 3, 06466, Gatersleben, Germany
 Tel: 039482-5522
 Fax: 039482-5595
 Email: stein@ipk-gatersleben.de
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most cases the EcoRI site is NOT present, as well as the
 EcoRI adapter used for cloning. To exist the insert,
 restriction sites upstream EcoRI should be used (e.g.,
 BamHI, SalI, PstI). NOTE: Also due to the cloning system
 used Blue/white selection for recombinants is not 100%
 reliable. Average insert size is 1.2 kb
 BASE COUNT 191 a 130 c 188 g 135 t
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 Query Match 47.88; Score 417.2; DB 14; Length 644;
 Best. Local Similarity 80.5%; Pred. No. 1,3e-118;
 Matches 488; Conservative 0; Mismatches 118; Indels 0; Gaps 0;
 Oy 35 GAAGTTCGCTCTTCTTCCACCCCGCAATCCATGAGAAACATTCAGATGTAA 94
 Db 35 GCATTTCTCGGAGAGACACTGCGGAGCGCCGCGCATGAGAAACGATTCGAGTGA 94
 Oy 95 GACGAGGTGATGAGAGATGGTACATGATGATGATGATGATGATGATGATGATG 154
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 1 (bases 1 to 709)
 Hedley, P., Liu, H., Caldwell, D., McCallum, N., Mudie, S., Cardie, L.,

TITLE Ramsay, L., Machray, G., Marshall, D.F.M. and Maugh, R.
JOURNAL Development of Barley Transcriptome Resources
COMMENT On Jan 10, 2002 this sequence version replaced g1:18113748.
Contact: Maugh R, Marshall DF
Genome Dynamics/Computational Biology
Scottish Crop Research Institute
Invergowrie, Dundee, DD2 5DA, Scotland, UK
Tel: 00 44 1382 562731
Fax: 00 44 1382 562426
Email: estescr@sari.ac.uk
All sequence has a phred quality score of 20 or over
Seq primer: M13 reverse.

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BASE COUNT 206 a 149 c 196 g 158 t
ORIGIN

Query Match 47.8%; Score 417.2; DB 13; Length 709;
Best Local Similarity 80.5%; Pred. No. 1,4e-118;
Matches 488; Conservative 0; Mismatches 118; Indels 0; Gaps 0;

OY 35 GAAGGTTGCTCTTCTTCACCCGCAATCCAGAGAGAAATTCAGATGTAA 94
DB 18 GCAGTCCGCGGAGACGTGCGAGGGCCGCCCATGTGAGAACGATTCAGATGCAA 77
OY 95 GACGAGGTGATAGAGATGTACATGATGATAGAGAGAGACCAAGGCTTCCTCA 154
DB 78 GGACGAGGTGATCCAGAGATGTACATGATGATGATGATGATGATGATGATGAT 137
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At
2
3